

SEARCH REQUEST FORM

Requestor's Name: _____ Serial Number: _____
Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

04/09/03 STAFF USE ONLY

Date completed:	04/09/03	Search Site	Vendors
Searcher:	Beverly e4994	STIC	IG Suite
Terminal time:	20	CM-1	STN
Elapsed time:		Pre-S	Dialog
CPU time:		Type of Search	APS
Total time:	28	N.A. Sequence	Geninfo
Number of Searches:		A.A. Sequence	SDC
Number of Databases:	11	Structure	DARC/Questel
		Bibliographic	Other CIGR

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STIC-Biotech/ChemLib

89679

From: Monshipouri, Maryam
Sent: Monday, March 24, 2003 9:47 AM
To: STIC-Biotech/ChemLib
Subject: case #09/719,748

Please interference search SEQ ID NO:1-2,
residues 1022-1141 of SEQ ID NO:1 ;and
residues 13-275 of SEQ ID NO:2.

Thank you.

Maryam Monshipouri Ph.D.
Primary Examiner
Art Unit 1652
Mail box No. 10D01

Point of Contact:
Beverly Shears
Technical Info. Specialist
CM1 1E05 Tel: 308-4994

RECEIVED
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(STIC)

Searcher: _____
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TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

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Monshirpour
D91719-748 Page 1
Seq. ID S-142 Inter

GenCore - version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on:

April 4, 2003, 19:24:37 ; Search time 5382.24 Seconds

(without alignments) 8137.548 Million cell updates/sec

Title: US-09-719-748-1

Perfect score: 1742

Sequence: 1 gaccggggcagtcgaccc.....aaacttctggtttacctgaa 1742

Scoring table: IDENTITY_NUC

Gapext 1.0

Searched: 24791104 seqs, 1271243825 residues

Total number of hits satisfying chosen parameters: 49582208

Minimum DB seq length: 0

Maximum DB seq length: 0

Post-processing: Minimum Match 0*

Maximum Match 100*

Listing first 45 summaries

Database : Pending Patents NA Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1742	100.0	1742	US-09-719-748-1
4	1730.4	99.3	2235	US-09-606-776-3799
5	1728.8	99.2	2235	US-09-643-163-9895
6	1728.8	99.2	2235	US-09-652-917-3775
7	1728.8	99.2	2235	US-09-698-010-12235
8	1728.8	99.2	2235	US-09-698-010-6041
9	1715.8	98.5	1970	US-60-270-232-3329
10	1042.2	59.8	1864	US-09-759-982-10
11	1032.4	59.3	1732	US-60-360-920-3361
12	1019.2	58.5	1512	US-09-649-163-7647
13	1019.2	58.5	1512	US-09-652-816-8022
14	1019.2	58.5	1512	US-09-652-911-8169
15	1019.2	58.5	1512	US-09-652-917-2793
16	1017.6	58.4	1451	US-09-277-2148-1776
17	1017.6	58.4	1451	US-09-891-825-176
18	1015	58.3	1253	PCT-US01-08631-9265
19	952	54.6	1198	US-09-652-914-8371
20	750.2	43.1	830	US-09-446-450
21	750.2	43.1	830	US-10-206-664-450

Result No.	Score	Query Match length	DB ID	Description
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23	750.2	43.1	830	US-10-206-664-450
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41	750.2	43.1	830	US-10-206-664-450
42	750.2	43.1	830	US-10-206-664-450
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Result No.	Score	Query Match length	DB ID	Description
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22 720.8 41.4 825 30 US-09-760-443-677 sequence 677, AP QY 241 GATCGAGGGAGGTGAGCACTCTCGGGAGCTCCTGCCACATGTCATCAGGTGCA 300
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 31 517.2 29.7 1096 25 US-09-652-913-9613 sequence 9613, AP Db 361 GCTCTTGATTCCTCGGCCAGAAGAGGAGTCATGAGTGGAGGAGGCCACAGCTCT 420
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 34 517.2 29.7 2079 23 US-09-652-917-2874 sequence 10274, AP Db 421 TRAGCAGATCTGGATGGGGAGACTACCTTACACAAAGAAATTGTCACATGT 480
 35 517.2 29.7 2201 71 US-60-278-258-3326 sequence 4326, AP QY 481 CGAGCGAGAACATATGTTAGACAGAAATTCCACACATCAAGCTGAT 540
 36 517.2 29.7 2231 61 US-60-172-373-4473 sequence 3737, AP QY 481 CGAGCGAGAACATATGTTAGACAGAAATTCCACACATCAAGCTGAT 540
 37 517.2 29.7 2384 23 US-09-606-776-3765 sequence 9484, AP QY 481 CGAGCGAGAACATATGTTAGACAGAAATTCCACACATCAAGCTGAT 540
 38 517.2 29.7 2387 25 US-09-652-125A-9484 sequence 8978, AP Db 481 CGAGCGAGAACATATGTTAGACAGAAATTCCACACATCAAGCTGAT 540
 39 517.2 29.7 2387 25 US-09-652-916-0429 sequence 10229, A QY 541 TGACTTGTCTGGCTACGAAATAGAGTGGAGTTGAGTGAATTTGGAC 600
 40 517.2 29.7 2387 25 US-09-652-917-3657 sequence 3157, AP QY 541 TGACTTGTCTGGCTACGAAATAGAGTGGAGTTGAGTGAATTTGGAC 600
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 42 517.2 29.7 2387 25 US-09-699-997-9047 sequence 9047, AP Sequence 6197, AP Db 541 TGACTTGTCTGGCTACGAAATAGAGTGGAGTTGAGTGAATTTGGAC 600
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ALIGNMENTS

RESULT 1
 PCT-US99-13411-1
 Sequence 1, Application PC/TUS9913411
 GENERAL INFORMATION:
 APPLICANT: KIMCHI, Adi
 APPLICANT: MCINNIS A., Patricia
 APPLICANT: YEDA RESEARCH AND DEVELOPMENT COMPANY LTD.
 TITLE OF INVENTION: DAP-KINASE RELATED PROTEIN
 FILE REFERENCE: KIMCHI2A
 CURRENT APPLICATION NUMBER: PCT/TUS99/13411
 CURRENT FILING DATE: 1999-06-15
 EARLIER APPLICATION NUMBER: 60/089,294
 EARLIER FILING DATE: 1998-06-15
 NUMBER OF SEQ ID NOS: 14
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 1
 LENGTH: 1742
 TYPE: DNA
 ORGANISM: Human
 FEATURE:
 LOCATION: (62)..(1141)
 PCT-US99-13411-1

Query Match 100.0%; Score 1742; DB 1; Length 1742;
 Best Local Similarity 100.0%; Pred. No. 0; Gaps 0;
 Matches 1742; Conservative 0; MisMatches 0; Indels 0;

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 Db 1 GACCGGGAGCTAGCCCTCCCGCGATGTTAGTTCCAGGCTCAATGAGGTCAA 60
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 QY 1561 TTGGGAAACGGGGATGAGAAGTGAACCTTGGGTGAGGACCAACTCTGACCT 1620
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 QY 1681 CCATGTCGCGCCCATTTGTAACCTCTGGTACATTATTAACCTCTGGTACCTG 1740
 Db 1681 CCATGTCGCGCCCATTTGTAACCTCTGGTACATTATTAACCTCTGGTACCTG 1740
 QY 1741 AA 1742
 Db 1741 AA 1742

RESULT 3
 US-09-719-748-1
 Sequence 1, Application US/09/19748
 GENERAL INFORMATION:
 APPLICANT: KIMCHI, Adi
 TITLE OF INVENTION: DAB-KINASE RELATED PROTEIN
 FILE REFERENCE: KIMCHI2A
 CURRENT APPLICATION NUMBER: US/09/719, 748
 CURRENT FILING DATE: 2000-12-15
 PRIOR APPLICATION NUMBER: 60/089, 294
 PRIOR FILING DATE: 1998-06-15
 NUMBER OF SEQ ID NOS: 14
 SOFTWARE: PatentIn ver. 2.0
 SEQ ID NO: 1
 LENGTH: 1742
 TYPE: DNA
 ORGANISM: Human
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (62)..(1141)
 US-09-719-748-1

Query Match 100.0% Score 1742; DB 28; Length 1742;
 Best Local Similarity 100.0%; Pred. No: 0;
 Matches 1742; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 GACCGGGGCACTGCTAGCTCCCGCGGATGTTGCTCCAGGCTCAATGAGGTCAA 60
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 Db 61 CATGGAGGCCATTCAAGGAGGAAGGGAGCTTATGATCATCGAGGAGCTGG 120
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 Db 61 CATGGAGGCCATTCAAGGAGGAAGGGAGCTTATGATCATCGAGGAGCTGG 120
 QY 121 GAGTGGCAGTTGCTCACTGAGAAGAGTCGGGGAGAGACGGCTGAGTATG 180
 Db 121 GAGTGGCAGTTGCTCACTGAGAAGAGTCGGGGAGAGACGGCTGAGTATG 180
 QY 1261 GAGATGGGCCAAGGAAATCAGAAGAGCTTGAGGCAAGCCAGGACCTGGGAGCTGT 1320

RESULT 4

US-09-606-776-3799

; Sequence 3799, Application US/09606776

; GENERAL INFORMATION:

; APPLICANT: Holtzman, Douglas A.

; APPLICANT: Myers, Paul

; APPLICANT: Gearing, David P.

; APPLICANT: Pan, Yang

TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES

FILE REFERENCE: 1600-1129-001

CURRENT APPLICATION NUMBER: US/09/606,776

CURRENT FILING DATE: 2000-06-27

PRIOR APPLICATION NUMBER: 60/141,578

PRIOR FILING DATE: 1999-06-29

PRIOR APPLICATION NUMBER: 60/141,379

PRIOR FILING DATE: 1999-06-28

PRIOR APPLICATION NUMBER: 60/141,138

PRIOR FILING DATE: 1999-06-28

PRIOR APPLICATION NUMBER: 60/141,581

PRIOR FILING DATE: 1999-06-29

NUMBER OF SEQ ID NOS: 5415

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 3799

LENGTH: 2235

TYPE: DNA

ORGANISM: Homo sapiens

US-09-606-776-3799

Query Match 99.3%; Score 1730.4; DB 23; Length 2235;

Best local similarity 99.7%; Pred. No. 0; Matches 1734; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 1 ACCCGGGCGACTCGCTCCCGGCGATTGATGTCAGCGCTTAATGGAGCTCAAC 60

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QY 1321 GGCGTCTCTCTGAGGGGCTCAGATCCAAAGCTCTTATTCCTCCATAAATGG 1380

Db 1321 GGCGTCTCTCTGAGGGGCTCAGATCCAAAGCTCTTATTCCTCCATAAATGG 1380

QY 1381 GCTTCCCTGTCGCCATCTCGAGCTGGGGAGTGAGCTAGGAAACAT 1440

Db 1381 GCTTCCCTGTCGCCATCTCGAGCTGGGGAGTGAGCTAGGAAACAT 1440

QY 1441 ATAAAGGACATCCATCATCATCACCGGGTGAAGGGTCAAGACTAAGCCAGCCTCTTACAGG 1500

Db 1441 ATAAAGGACATCCATCATCACCGGGTGAAGGGTCAAGACTAAGCCAGCCTCTTACAGG 1500

QY 1501 CTGGGGGCTTCAGAACCGCTGCCAAATAACCCAGAGAACAGAGTCTCC 1560

Db 1501 CTGGGGGCTTCAGAACCGCTGCCAAATAACCCAGAGAACAGAGTCTCC 1560

QY 1561 TTGGACACGGGTATGAGGAAGTGAACCTGGTGTAGGGACCAATCTCTGACCT 1620

Db 1561 TTGGACACGGGTATGAGGAAGTGAACCTGGTGTAGGGACCAATCTCTGACCT 1620

QY 1621 CCCGAAACCATGGAGCCAGGACCTCAGCTGACCAACCTCGACCTCTGAGCAGC 1680

Db 1621 CCCGAAACCATGGAGCCAGGACCTCAGCTGACCAACCTCGACCTCTGAGCAGC 1680

QY 1681 CCATGCTGCCCATGTTGATTTGCTCTTTTAACACTCTGTTACCTG 1740

Db 1681 CCATGCTGCCCATGTTGATTTGCTCTTTTAACACTCTGTTACCTG 1740

QY 1741 AA 1742

Db 1741 AA 1742

QY 62 ATGGAGCCATTCAAGCAGCAGAAGGTGAGGACTTTATGACATCGAGAGAGAGCTGG 121

Db 61 ATGGAGCCATTCAAGCAGCAGAAGGTGAGGACTTTATGACATCGAGAGAGCTGG 120

QY 122 ATGGCCAGTTGCATCTGAGAAGAGTCCGGAGAAGAGCAGGGGTCTGAGTATGCA 181

Db 122 ATGGCCAGTTGCATCTGAGAAGAGTCCGGAGAAGAGCAGGGGTCTGAGTATGCA 181

QY 182 GCGAAGTTCATCAAGAACGGCGAGGCCCGGAGGAGCTGAGCTTATGACATCGAGAGCTGG 241

Db 182 GCGAAGTTCATCAAGAACGGCGAGGCCCGGAGGAGCTGAGCTTATGACATCGAGAGCTGG 240

QY 242 ATCGAGCGAGGTGAGCATCCCTGGGAGGCTGAGCTGACCCATGTCATCAGCTGAC 301

Db 241 ATCGAGCGAGGTGAGCATCCCTGGGAGGCTGAGCTGACCCATGTCATCAGCTGAC 300

QY 302 GACGTCTATGAGAACCGCAGCGAGCTGGTGCAGCTCTGAGTAGTCTGGAGGAG 361

Db 301 GACCTCTATGAGAACCGCAGCGAGCTGGTGCAGCTCTGAGTAGTCTGGAGGAG 360

QY 362 CTCTTCGATTCTCTGGCCAGAACGGAGGCTCATGAGTGGAGGAGGAGGCTTCACTT 421

Db 361 CTCTTCGATTCTCTGGCCAGAACGGAGGCTCATGAGTGGAGGAGGAGGCTTCACTT 420

QY 422 AASERGATCTGGATGGGGTAACCTACCTTACACATCGACCTCTGTCATCTTGACTC 481

Db 421 AASERGATCTGGATGGGGTAACCTACCTTACACATCGACCTCTGTCATCTTGACTC 480

QY 482 AAGCAGAAACATTATGTTGAGACAGAAATTCCCATCACACATCAAGTATT 541

Db 481 AAGCAGAAACATTATGTTGAGACAGAAATTCCCATCACACATCAAGTATT 540

QY 542 GACTTTGGCTTGGCTACAGAAATAGAGATGGAGTTGAGATTAGAAATTTTGGACG 601

Db 541 GACTTTGGCTTGGCTACAGAAATAGAGATGGAGTTGAGATTAGAAATTTTGGACG 600

QY 602 CCGAAATTGTTGCTCAGAAATTGTAACCTAGAGCCCTGGCTCGAGAGCTGACATG 661

Db 601 CCGAAATTGTTGCTCAGAAATTGTAACCTAGAGCCCTGGCTCGAGAGCTGACATG 660

QY 662 TGGACATGGCTCATCACATCAGCTCTTAACTGGAGCATCCCTTCTGGAGAC 721

Db 661 TGGACATGGCTCATCACATCAGCTCTTAACTGGAGCATCCCTTCTGGAGAC 720

QY 722 ACGAGCAGGAAACACTGCCAAATATCACATCAGTCACTGAGTTACCTTGATGAGGAATTC 781

Db 721 ACGAGCAGGAAACACTGCCAAATATCACATCAGTCACTGAGTTACCTTGATGAGGAATTC 780

QY 782 TTCAGCCATAGGAGCGACCTGGCAAGAACCTTATCGAGCTCAGCTTGTAAAGAGAC 841

Db 781 TTCAGCCATAGGAGCGACCTGGCAAGAACCTTATCGAGCTCAGCTTGTAAAGAGAC 840

QY 842 CGGAAACGCCACATCCAGAGGGCTCTAGACACCCCTGGATCACCGGGTGGACAC 901

Db 841 CGGAAACGCCACATCCAGAGGGCTCTAGACACCCCTGGATCACCGGGTGGACAC 900

QY 902 CAGGAGCCATGGTGCAGCGAGCTCTGTCATCTGAGACTTCAGGAGCAGT 961

Db 901 CAGGAGCCATGGTGCAGCGAGCTCTGTCATCTGAGACTTCAGGAGCAGT 960

QY 962 GTCCGCAAGGGCTTCAGGAGGACTTCCTTCAGGAGGCTTCAGGAGGACTTCAGGAGCAGT 1021

Db 961 GTCCGCAAGGGCTTCAGGAGGACTTCCTTCAGGAGGACTTCAGGAGCAGT 1020

QY 1022 TCGCTGAGAGAGGAGGCTTCAGGAGGACTTCCTTCAGGAGGACTTCAGGAGCAGT 1081

Db 1021 TCGCTGAGAGAGGAGGCTTCAGGAGGACTTCCTTCAGGAGGACTTCAGGAGCAGT 1080

QY 1082 ACTCGAGGAGCATGCCAGGAGAACCCCTCACCCACGGAGGAGGAGCACCTCC 1141

Db 1081 ACTCGAGGAGCATGCCAGGAGAACCCCTCACCCACGGAGGAGGAGCACCTCC 1140

QY 1142 TAACTGGCTGACCTGCAGTGGCCAGGGAGGTTGGGCCAGGGCTCCCTCTG 1201

Matches 1733; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY	1022	TCGGTGATGAGAGGTCACCTGAGCCGGATGAGGACTCTGAGAGTGC	1081
Db	1021	TGCTGTGATGAGAGGTCACCTGAGGACTCTGAGAGTGC	1080
QY	1082	ACTGGAGGAGCATGCCAGGAGAACCCCTCCACCGACGAGGAGCTGAGGAGTGC	1141
Db	1081	ACTGGAGGAGCATGCCAGGAGAACCCCTCCACCGACGAGGAGTGC	1140
QY	1142	TACTCGCTGACTCTGAGCTGGCCCGCCGGAGCTTGGGCCAGGGGCTCCCTCTG	1201
Db	1141	TACTCGCTGACTCTGAGCTGGCCCGCCGGAGCTTGGGCCAGGGGCTCCCTCTG	1200
QY	1202	TGCAAGCTTGGACCCAGCTGAGCTGAGCCACCGACGGGGCTCTGAGAG	1261
Db	1201	TGCAAGCTTGGACCCAGCTGAGCTGAGCCACCGACGGGGCTCTGAGAG	1260
QY	1262	AGATGGCCCAAGGAATTAGAGGCTCAGGGAGCCCTGGAGGACTCTGGAGTGC	1321
Db	1261	AGATGGCCCAAGGAATTAGAGGCTCAGGGAGCCCTGGAGGACTCTGGAGTGC	1320
QY	1322	GTCTCTCTCTGGAGGAGGTCACGATCCTCAAAGCTCTTAATCTCCATAATGG	1381
Db	1321	GTCTCTCTCTGGAGGAGGTCACGATCCTCAAAGCTCTTAATCTCCATAATGG	1380
QY	1382	CTTCCTCTGCTGCCATCTCAGAGCTCTGGGGTGGGAGTGTGACTTAGGAAATA	1441
Db	1381	CTTCCTCTGCTGCCATCTCAGAGCTCTGGGGTGGGAGTGTGACTTAGGAAATA	1440
QY	1442	TAAGGACATCCATCATCACGGGTGAAGTCACTGAGCTTCAAGGAGCTTCAGGC	1501
Db	1441	TAAGGACATCCATCATCACGGGTGAAGTCACTGAGCTTCAAGGAGCTTCAGGC	1500
QY	1502	TGAGGGGTCAAGACCCCTGCCAAATAATCACCAAGGAGCAAGAGTCTCCAT	1561
Db	1501	TGAGGGGTCAAGACCCCTGCCAAATAATCACCAAGGAGCAAGAGTCTCCAT	1560
QY	1562	TGGACACGGGTGATGAGGAATCTGGGTGAGGACCATCTCTGAGCTC	1621
Db	1561	TGGACACGGGTGATGAGGAATCTGGGTGAGGACCATCTCTGAGCTC	1620
QY	1622	CCAGAACATGGAGCCAGGTCAGGTGACAAACCTGACTCTGAGCTTGAGAGC	1681
Db	1621	CCAGAACATGGAGCCAGGTCAGGTGACAAACCTGACTCTGAGCTTGAGAGC	1680
QY	1682	CATTGCTGCCCACTGTTAATTTGCTCTTTAACTCTGGTTACCTGA	1741
Db	1681	CATTGCTGCCCACTGTTAATTTGCTCTTTAACTCTGGTTACCTGA	1740

RESULT 7

US-09-698-010-12235

; Sequence 12235, Application US/09698010

; GENERAL INFORMATION:

; APPLICANT: Williamson, Mark

; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES

; FILE REFERENCE: 1500.2029-001

; CURRENT APPLICATION NUMBER: US/09/698 010

; CURRENT FILING DATE: 2000-10-27

; PRIOR APPLICATION NUMBER: 60/162,358

; PRIOR FILING DATE: 1999-10-29

; NUMBER OF SEQ ID NOS: 15684

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 12235

; LENGTH: 2235

; TYPE: DNA

; ORGANISM: Homo sapiens

Query Match 99.2%; Score 1728.0; DB 27; Length 2235;

Best Local Similarity 99.6%; Pred. No. 0;

US-09-698-010-12235

QY 1082 ACTGAGGAGACATGCCAGGAGAAAGCCCTCACCCAGGAGGAGGAGGACCTCC 1141
 Db 1081 ACTGGAGGAGACATGCCAGGAGAAAGCCCTCACCCAGGAGGAGGACCTCC 1140
 QY 1142 TAACTGGCCTGACCTGCACTGGCCAGGGAGTTGGCCCGCAGGGAGGCTCG 1201
 Db 1141 TAACTGGCCTGACCTGCACTGGCCAGGGAGGCTCG 1200
 QY 1202 TGCAGACTTTGGAGCCAGCTCAGACACAGCACCGAGGCTCG 1261
 Db 1201 TGCAGACTTTGGAGCCAGCTCAGACACAGCACCGAGGCTCG 1260
 QY 1262 AGATGGGCCAAGGAAATTCAAGAGAGCTGCAAGGGAGCCAGGAGGACCTTG 1321
 Db 1261 AGATGGGCCAAGGAAATTCAAGAGAGCTGCAAGGGAGCCAGGAGGACCTTG 1320
 QY 1322 GCTGTCTCTGTGGAGGAGGCTCCAGATTCCTCCAGTCAGTCTTAAATTCTCCATAAATGG 1381
 Db 1321 GCTGTCTCTGTGGAGGAGGCTCCAGATTCCTCCAGTCAGTCTTAAATTCTCCATAAATGG 1380
 QY 1382 CTTCCTCTGTCGCCATCTCAGACTGGGGAGGTTGAGACTTAGGAAACATA 1441
 Db 1381 CTTCCTCTGTCGCCATCTCAGACTGGGGAGGTTGAGACTTAGGAAACATA 1440
 QY 1442 TAAGGACATCTCATCATCACGGGTGAGGTAGAGTAAGGAGCCCTTCACGGC 1501
 Db 1441 TAAGGACATCTCATCATCACGGGTGAGGTAGAGTCAGGAGCCCTTCACGGC 1500
 QY 1502 TGAGGGGGTCTCAGAACACAGCCTGGCCAAAATTACACAGAGACAGAGTCCTCCCAT 1561
 Db 1501 TGAGGGGGTCTCAGAACACAGCCTGGCCAAAATTACACAGAGACAGAGTCCTCCCAT 1560
 QY 1562 TGGGACAGGGTGTGAGGAAGTGAACCTTGAGGAGGACCAATCTCTGACCTC 1621
 Db 1561 TGGGACAGGGTGTGAGGAAGTGAACCTTGAGGAGGACCAATCTCTGACCTC 1620
 QY 1622 CCAGAACCTGGAGGCCAGGAGCTGACCTTGAGGAGGACCACTTGAGGAGCC 1681
 Db 1621 CCAGAACCTGGAGGCCAGGAGCTGACCTTGAGGAGGACCACTTGAGGAGCC 1680
 QY 1682 CATGGCTGCCGCCATGTGTAAATTGCTCATTTTAAACTCTGGTTACCTGA 1741
 Db 1681 CATGGCTGCCGCCATGTGTAAATTGCTCATTTTAAACTCTGGTTACCTGA 1740

RESULT 8

Sequence 6041, Application US/09698013

GENERAL INFORMATION:

APPLICANT: Gearring, David P.

APPLICANT: Comrack, Christopher

APPLICANT: Kingsbury, Gillian A.

APPLICANT: Holtzman, Douglas A.

TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES

TITLE OF INVENTION: THEREFOR

FILE REFERENCE: 1600_2013-001

CURRENT APPLICATION NUMBER: US/09/698, 013

CURRENT FILING DATE: 2000-10-27

PRIOR APPLICATION NUMBER: 60/162, 360

PRIOR FILING DATE: 1999-10-29

NUMBER OF SEQ ID NOS: 735

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 6041

LENGTH: 2235

TYPE: DNA

; ORGANISM: Homo sapiens

; US-09-698-013-6041

Query Match 99.2% Score 1728.8; DB 27; Length 2235;

Best Local Similarity 99.6%; Pred. No. 0; Mismatches 7; Indels 0; Gaps 0;

Matches 1713; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Db 61 ATGGAGCATTCAAGAGCAAGGGAGGACTTTATGACATCGGAGAGGAGCTGAGTC 120
 Db 61 ATGGAGCATTCAAGAGCAAGGGAGGACTTTATGACATCGGAGAGGAGCTGAGTC 121
 QY 122 AGTGGCCAGTTGGCATGTGAAGAAGTGTGCGCCGGAGGAGGAGCTTGATGATC 181
 Db 121 AGTGGCCAGTTGGCATGTGAAGAAGTGTGCGCCGGAGGAGGAGCTTGATGATC 180
 QY 182 GCGMAGTTATCGAAGAGCCGAGAGCGGGAGGAGCCGGGGCTGAGCCGGAGG 241
 Db 181 GCGMAGTTATCGAAGAGCCGAGAGCGGGAGGAGCCGGGGCTGAGCCGGAGG 240
 QY 242 ATCGAGCGGGAGGTTGAGATCTGGGGAGGTTGAGCTGAGCCATGTCATCAGCTGAC 301
 Db 241 ATCGAGCGGGAGGTTGAGATCTGGGGAGGTTGAGCTGAGCCATGTCATCAGCTGAC 300
 QY 302 GACCTCTATGAGACCGAACCGAGCTGTTGAGGAGGTTGAGCTGAGCTGAGGAG 361
 Db 301 GACCTCTATGAGACCGAACCGAGCTGTTGAGGAGGTTGAGCTGAGCTGAGGAG 360
 QY 362 CTCTCTGATTCTGGCCAGAGGAGCTGAGTGGAGGAGGACACGCTTCATT 421
 Db 361 CTCTCTGATTCTGGCCAGAGGAGCTGAGTGGAGGAGGACACGCTTCATT 420
 QY 422 AAGGAGATCTGGATGGGGTGAACACTTACCTTACACACATTCAGTGTGATT 481
 Db 421 AAGGAGATCTGGATGGGGTGAACACTTACCTTACACACATTCAGTGTGATT 480
 QY 482 AASCAGAGAACATATTATGTTAGACAGAAATTCCATTCACACATTCAGTGTGATT 541
 Db 481 AAGCCAGAGAACATATTATGTTAGACAGAAATTCCATTCACACATTCAGTGTGATT 540
 QY 542 GACTTGTTCTGCTCAGAAATTAGAGATGGAGTGAATTAGAATATTGAGC 601
 Db 541 GACTTGTTCTGCTCAGAAATTAGAGATGGAGTGAATTAGAATATTGAGC 600
 QY 602 CCGGAATTGTTGCTCCAGAAATTGTAACCTAGAGCCCTGGCTGGAGGCTGACATG 661
 Db 601 CCGGAATTGTTGCTCCAGAAATTGTAACCTAGAGCCCTGGCTGGAGGCTGACATG 660
 QY 662 TGGGACATGGGCTCATCACCATCACATCTCTTAAGTGGAGCATCCCTTCTGGAGAC 721
 Db 661 TGGGACATGGGCTCATCACCATCACATCTCTTAAGTGGAGCATCCCTTCTGGAGAC 720
 QY 722 ACGAGACGGAAACATGGCAATTACATCACATCTGAGTTAGCTTGAGGAATC 781
 Db 721 ACGAGACGGAAACATGGCAATTACATCACAGCTGAGTTAGCTTGAGGAATC 780
 QY 782 TTGAGCCATACAGGAGGAGCTGGCCAAGGACTTATTGGAGCTGAGTTAGGAAATC 841
 Db 781 TTGAGCCATACAGGAGGAGCTGGCCAAGGACTTATTGGAGCTGAGTTAGGAAATC 840
 QY 842 CGGAAACCGGTCACAATCAGAGGCTGCAACCTTGAGTACGGCCGGTGGACAC 901
 Db 841 CGGAAACCGGTCACAATCAGAGGCTGCAACCTTGAGTACGGCCGGTGGACAC 900
 QY 902 CACCAAGCATGTGGAGGAGGACTTGAGTACGGAGACTTCAGGAGAGCT 961
 Db 901 CACCAAGCATGTGGAGGAGGACTTGAGTACGGAGACTTCAGGAGAGCT 960
 QY 962 GTCGCAGGGTGGAGGACTTGAGTACGGAGACTTCAGGAGACTTCAGGAGAGCT 1021
 Db 961 GTCGCAGGGTGGAGGACTTGAGTACGGAGACTTCAGGAGACTTCAGGAGAGCT 1020
 QY 1022 TCGCTGATGAGAGGAGTCACCTGAGGAGGACTTGAGTACGGAGACTTCAGGAGAGCT 1081
 Db 1021 TCGCTGATGAGAGGAGTCACCTGAGGAGGACTTGAGTACGGAGACTTCAGGAGAGCT 1080
 QY 1082 ACTGAGGAGACATGCCAGGAGAAAGCCCTCACCCAGGAGGAGGAGGACCTCC 1141

Db 1081 ACTGGAGGACATGCCAGGAAAGCCCTCCACCCACGGAGGAGGAGCCTCC 1140
 Qy 1142 TAATGGCTGACCTGCAGCTGGGCCAGGGAGGTTGGGCCAGGGGCTCCCTCTG 1201
 Db 1141 TAATGGCTGACCTGCAGCTGGGCCAGGGAGGTTGGGCCAGGGGCTCCCTCTG 1200
 Qy 1202 TGCAGACTTGGACCCAGCTCACCCACCGACCCGGACGGTCTGACACTTGAGAG 1261
 Db 1201 TGCAGACTTGGACCCAGCTCACCCACCGACCCGGTCTGAGACTTGAGAG 1260
 Qy 1262 AGATGGGCCAAGGAAATTGAGGAGGCTCACCCACCGACCCGGTCTGAGAG 1321
 Db 1261 AGATGGGCCAAGGAAATTGAGGAGGCTCACCCACCGACCCGGTCTGAGAG 1320
 Qy 1322 GCTGCTCTCTGAGGAGGCTCACCCACCGACCCGGTCTGAGACTTGAGAG 1381
 Db 1321 GCTGCTCTCTGAGGAGGCTCACCCACCGACCCGGTCTGAGACTTGAGAG 1380
 Qy 1382 CTTCCCTGCTGCTGCATCTCGAGCTCGAGCTCGGGTGGAGCTAGAAGCTA 1441
 Db 1441 TAAGGACATCCATCTCGAGCTCGGGTGAAGGTCAAGCTAGAAGCTA 1440
 Db 1381 CTTCCCTGCTGCTGCATCTCGAGCTCGGGTGGAGCTAGAAGCTA 1440
 Qy 1442 TAAAGGACATCTCATCGAGCTCGGGTGAAGGTCAAGCTAGAAGCTA 1500
 Db 1502 TGGGGGGTCAACACCGCCAAATTACACCAACCTGAGCTCGGGTCTCCCAT 1561
 Db 1501 TGGGGGGTCAACACCGCCAAATTACACCAACCTGAGCTCGGGTCTCCCAT 1560
 Qy 1562 TGGGACACGGGTCACTGGAGGAGCTGGGGTGGGGCAATCTGTACCTC 1621
 Db 1561 TGGGACACGGGTCACTGGAGGAGCTGGGGTGGGGCAATCTGTACCTC 1620
 Qy 1622 CCAGAACCTGGAGGCCAGGAGCTGGAGGAGCTGGGGTGGGGCAATCTGTACCTC 1681
 Db 1621 CCAGAACCTGGAGGCCAGGAGCTGGGGTGGGGCAATCTGTACCTC 1680
 Qy 1682 CAGTGTGACCCGCACTGTGTATTGCTCACTTATTAACCTCTGTGTACTGA 1741
 Db 1681 CATTGCTGGCCGCACTGTGTATTGCTCACTTATTAACCTCTGTGTACTGA 1740

RESULT 9
 US-60-278-232-3329
 ; sequence 3329 Application US/60278232
 ; GENERAL INFORMATION:
 ; APPLICANT: Lal Preeti
 ; APPLICANT: Morris Macdonald
 ; APPLICANT: Lal Preeti
 ; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
 ; Polymorphic Sequence Databases, and Single Nucleotide
 ; Polymorphisms Identified Thereby
 ; TITLE OF INVENTION: Polymorphic Sequence Databases, and Single Nucleotide
 ; FILE REFERENCE: GK-0011_P
 ; CURRENT APPLICATION NUMBER: US/60/278, 232
 ; CURRENT FILING DATE: 2001-03-30
 ; NUMBER OF SEQ ID NOS: 12,557
 ; SOFTWARE: PERL program
 ; SEQ ID NO: 3329
 ; LENGTH: 1970
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE: misc_feature
 ; NAME/KEY: misc_feature
 ; OTHER INFORMATION: Incyte ID No: 211168.4
 ; US-60-278-232-3329

Query Match 99.5%; Score 1715.8; DB 71; Length 1970;
 Best Local Similarity 99.4%; Pred. No. 0; Mismatches 7; Indels 4; Gaps 1;
 Matches 1734; Conservative 0; Mismatches 7; Indels 4; Gaps 1;
 1 GACCGGGCAGCTAGCCCTCCGGGATTTGTCAGGCTCATGGAGAGTCAAA 60

Db 12 GACCCGGCAGGTCACTCCGGCCATTGTTCAAGGAGTCAAA 71
 Qy 61 CATGGAGGCAATTCAAGCAGCAGAGGGACTTTATGACATGGAGAGGAGCTGG 120
 Db 72 CATGGAGCATTCAAGCAGCAGAGGGAGGACTTTATGACATGGAGAGGAGCTGG 131
 Qy 121 GAGTGGCGRTTGTGCTGCATGAGAAGAGAGACACGGGCTTGACTATGC 180
 Db 132 GAGTGGCGRTTGTGCTGCATGAGAAGAGAGACACGGGCTTGACTATGC 191
 Qy 181 AGCCAGTTCAAGAAGCAGCCGGGAGGGAGGAGACACGGGCTTGACTATGC 251
 Db 192 AGCCAGTTCACTAGAAGAGGAGGAGGAGGAGGAGACACGGGCTTGACTATGC 300
 Qy 241 GATCAGGGGGAGGTGACATCTGCGCAGGTGCTGCGCAGGCTGACAGCTGCA 311
 Db 252 GATCAGGGGGAGGTGACATCTGCGCAGGTGCTGCGCAGGCTGACAGCTGCA 311
 Qy 301 CGACGCTATGAGAACCGCACGGCTGTGACATCTTGTGCTAGTGTCTGGAGGA 360
 Db 312 CGACGCTATGAGAACCGCACGGCTGTGACATCTTGTGCTAGTGTCTGGAGGA 371
 Qy 361 GCTCTTGATTCCTGGCCAGGAGGAGCTGAGCTGCTGCGCAGGAGGAGCAGCTGCA 420
 Db 372 GCTCTTGATTCCTGGCCAGGAGGAGCTGAGCTGCTGCGCAGGAGGAGCAGCTGCA 431
 Qy 421 TAAGCAGATCTGGAGGGGGAACCTACCTTACACAAAGAAATTGCTCACTTGACT 480
 Db 432 TAAGCAGATCTGGAGGGGGAACCTACCTTACACAAAGAAATTGCTCACTTGACT 491
 Qy 481 CGACGCTATGAGAACCTTACACAAAGAAATTCCATCCACACATCAAGCTGAT 540
 Db 492 CAAGCCGAAACATTAATGTTAGACAGAAATTCCATCCACACATCAAGCTGAT 551
 Qy 541 TCACTTGTCTGGCTCAGGAATAGAAGATGGAGTGTGAATTAAAGAATTTTGGAC 600
 Db 552 TCACTTGTCTGGCTCAGGAATAGAAGATGGAGTGTGAATTAAAGAATTTTGGAC 611
 Qy 601 GCGGAATTGTTGCTCAGGAATTTGAGACTACAGGCCCTGGGCTGGGGCTGACAT 660
 Db 612 GCGGAATTGTTGCTCAGGAATTTGAGACTACAGGCCCTGGGCTGGGGCTGACAT 671
 Qy 661 GTGGGACATAGGGTCATCACTACATCTTAACTGGACATCCCTTCTGGAGA 720
 Db 672 GTGGGACATAGGGTCATCACTACATCTTAACTGGACATCCCTTCTGGAGA 731
 Qy 721 CACGAGCAGAACACTGGCAATATCACATCGAGTGTACGCTTGTGAGGATT 780
 Db 732 CACGAGCAGAACACTGGCAATATCACACAGCTGAGTGTACGCTTGTGAGGATT 791
 Qy 781 CTTCACTGGCTCACGAGCTGGCAAGGAGCTTATCGGAAGCTCTGGTAAGGAC 840
 Db 792 CTTCACTGGCTCACGAGCTGGCAAGGAGCTTATCGGAAGCTCTGGTAAGGAC 851
 Qy 841 CGGAACGCTCAATCCAAAGGGCTCACGAGCTGGCAAGGAGCTTATCGGAAGCTCTGGTAAGGAC 900
 Db 852 CGGAACGCTCACGAGCTGGCAAGGAGCTTATCGGAAGCTCTGGTAAGGAC 911
 Qy 901 CCAGCAACCTGGCGACGGAGCTCTGGCAAGGAGCTTATCGGAAGCTCAAGGAGCTA 960
 Db 912 CCAGCAACCTGGCGACGGAGCTCTGGCAAGGAGCTTATCGGAAGCTCAAGGAGCTA 971
 Qy 1021 CTCGCTGATGAGAAGGTGAGCTGAGGAGGATGGACTTGGAGACTTCAGGAGCTA 1020
 Db 1032 CTCGCTGATGAGAAGGTGAGCTGAGGAGGATGGAGACTTCAGGAGCTTCAGGAGCTA 1031
 Qy 1077 GTGACACTGAGGAGGACATCCAGGAGGAAGCCCTCAACCCAGGAGGAGGAGCA 1136

Query Match 59.8%; Score 1042.2; DB 29; Length 1864;
 Best Local Similarity 99.2%; Pred. No. 2.8e-245; Mismatches 8; Indels 0; Gaps 0;
 Matches 1047; Conservative 0; Name/Key: CDS; Location: (275)..(754); US-09-757-982-10

Db 1092 GTGACACTGAGGGAGACATGCCGGAGAAASCCCTCACCCCGAGGAGGAGCACCA 1151 Qy 687 TCCCTTAAGTGGAGCATCCCTTCMGGAGACAGAGCGAACATCGCAATA 746
 Qy 1137 CCTCTTAACCTGGGCTGACCTGAGCGCCACGGAGTTGGCCCTGGGGCTCC 1196 Db 300 TCACTTAAGTGGAGCATCCCTTCMGGAGACAGAGCGAACATCGCAATA 359
 Db 1152 CCTCTTAACCTGGGCTGACCTGAGCGCCACGGAGTTGGCCCTGGGGCTCC 1211 Qy 747 TCACTCATGAGTTACGACTTGTAGGAAATCTTCAGCCATACGGAGCTGGCA 806
 Qy 1197 TTCTGTGAGACTTTGGGCCACTCGAGCGACCGGTTGGCCCTGGGGCTCC 1256 Db 360 TCACTCATGAGTTACGACTTGTAGGAAATCTTCAGCCATACGGAGCTGGCA 419
 Db 1212 TTCTGTGAGACTTTGGGCCACTCGAGCGACCGGTTGGCCCTGGGGCTCC 1271 Qy 807 AGGACTTATCGAGCTTGTGGTTAAAGAGACCGGAAACCGCTCACATTCAGG 866
 Qy 1257 AAGGAGATGGCCCAAGGAAATTAGAGAGCTTGAGGAAGGAGCCCTGGAG 1316 Db 420 AGGACTTATCGAGCTTGTGGTTAAAGAGACCGGAAACCGCTCACATTCAGG 479
 Db 1272 AAGGAGATGGCCCAAGGAAATTAGAGAGCTTGAGGAAGGAGCCCTGGAG 1331 Qy 867 CTCTCAGGACCCCTGGATACCCCGTGGAGACACCGAACCATGTCGAGGGT 926
 Qy 1317 CTGAGGCTGCTCTGTGGAGGAGCTCCAGATCCAGATTCAGGACCTTTC 1376 Db 480 CTCTCAGGACCCCTGGATACCCCGTGGAGACACCGAACCATGTCGAGGGT 539
 Db 1332 CTGAGGCTGCTCTGTGGAGGAGCTCCAGATTCAGGACCTTTCATATA 1391 Qy 927 CTGAGGCTGAGCTGGAGAACTTGGAGAAGGAGTGTGGAGTGGAGCTTCT 986
 Qy 1377 ATSGCTTCTCTGCTGCTGAGGAGCTCCAGATCCAGATTCAGGACCTTTC 1436 Db 540 CTGAGGCTGAGCTGGAGAACTTGGAGAAGGAGTGTGGAGTGGAGCTTCT 599
 Db 1392 ATGGCTTCTCTGCTGCTGAGGAGCTCCAGATTCAGGACCTTTCATATA 1451 Qy 987 TCAGCATCGACCCCTGGATACCGGGTTGGAGACAGACACCGAACCATGTC 1046
 Qy 1437 CAATTAAGGACCTCTCATCATCACGGGTGAGGTGAGGAGCTCTTC 1496 Db 600 TCAGCATCGTCCTGTGCAACACCCTCACCGCTCGTGTGAGAGGAGCTTCT 659
 Db 1452 CAATTAAGGACCTCTCATCATCACGGGTGAGGTGAGGAGCTCTTC 1511 Qy 1047 GGGCGATGAGGAGCTGGAGACTTCAGGAGAGTGTGGAGACACTGAGGG 1106
 Qy 1497 CAGGCTGAGGGGGTCAGAACACCTGGCAAATAATTACACCHAGAGACAG 1556 Db 660 GGCAGGATGAGGAGCTGGCTTC 719
 Db 1512 CAGGCTGAGGGGGTCAGAACACCTGGCAAATAATTACACCHAGAGACAG 1571 Qy 1107 AAGCCCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1166
 Qy 1557 CCCATGGGACACGGTGTGAGGAAGTGAACCTGGGTGAGGACCATCTG 1616 Db 720 AAGCCCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 779
 Qy 1572 CCCATGGGACACGGTGTGAGGAAGTGAACCTGGGTGAGGACCATCTG 1631 Db 840 ACCAGACCGGGGCTCCCTGACACTTGTGAGGAGATGGACCATGGGG 899
 Db 1617 ACCTCCAGAACCTGGAAAGCCAGGAGCTGGTGGAGAACACCTGAGG 1676 Db 780 CCAGGGAGCTGGGCCAGGGGGCTCCCTGTGAGGAGCTTGGAGCTTGG 839
 Db 1632 ACCCTCCAGAACCTGGAAAGCCAGGAGCTGGTGGAGAACACCTGAGG 1691 Qy 1227 ACCGGACCCGGGCTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1286
 Qy 1677 CAGGCCATGCTGCCGCCATGTGTAATTCTCATTTTATAACTTCMGGTT 1736 Db 840 ACCAGACCGGGGCTCCCTGACACTTGTGAGGAGATGGACCATGGGG 1226
 Db 1692 CAGGCCATGCTGCCGCCATGTGTAATTCTCATTTTATAACTTCMGGTT 1751 Qy 1287 GCTTGAGGAGCCAGGAGGAGGACCTGGAGCTGGCTGTCTGTGGAGGGCTCA 1346
 Qy 1737 CCTGA 1741 Db 900 GCTTGAGGAGCCAGGAGGACCTGGAGCTGGCTGTCTGTGGAGGGCTCA 959
 Db 1752 CCTGA 1756 Qy 1347 GCATTCAGGAAAGCTTAAATCTCCATATAATGGCTTCTCTGTGCTGCA 1406
 . RESULT 10
 . US-09-757-982-10
 . Sequence 10.. Application US/09757982
 . GENERAL INFORMATION:
 . APPLICANT: Acton, Susan
 . TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
 . FILE REFERENCE: MNI-050
 . CURRENT APPLICATION NUMBER: US/09/57,982
 . CURRENT FILING DATE: 2001-01-10
 . PRIOR APPLICATION NUMBER: 09/163,115
 . PRIOR FILING DATE: 1998-09-29
 . NUMBER OF SEQ ID NOS: 15
 . SOFTWARE: PatentIn Ver. 2.0
 . SEQ ID NO 10
 . LENGTH: 1864
 . TYPE: DNA
 . ORGANISM: Homo sapiens
 . FEATURE:
 . NAME/KEY: CDS
 . LOCATION: (275)..(754)

RESULT 11
 US-09-719-748-1.rnpm
 : Sequence 3361, Application US/60360207
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig
 ; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
 ; FILE REFERENCE: C101321
 ; CURRENT APPLICATION NUMBER: US 60/360,207
 ; CURRENT FILING DATE: 2002-03-01
 ; NUMBER OF SB0 ID NOS: 47235
 ; SEQ ID NO 3361
 ; LENGTH: 1732
 ; TYPE: DNA
 ; ORGANISM: HUMAN
 ; US-09-719-748-1.rnpm
 Query Match 59.3%; Score 1032.4; DB 80; Length 1732;
 Best Local Similarity 83.8%; Pred. No. 7e-243; DB 80; Length 1732;
 Matches 1263; Conservative 0; Mismatches 186; Indels 59; Gaps 6;
 Qy 8 GCGCTCAGCTCCCGCGATGTTGATGTCAGGCTCAAGCTGAGTCAAAGATGG 67
 Db 91 GCGCGCGAGCCCTTCGCGATGTTGATGTCAGGCTCAAGCTGAGTCAAAGATGG 150
 Qy 128 CAGTTGCATGTTGAGAGTCCCGGGAGAGAGACCGGGCTGAGATGCGCCAAG 187
 Db 211 CAGTTGCATGTTGAGAGACCGGGCTGAGAGACCGGGCTGAGATGCGCCAAG 270
 Qy 68 CCGTTCAGCAGCAGAGGTGGACTTTATGACATCGAGGGAGCTGGAGTGG 127
 Db 151 AGCTTCACACAGCAGAGGTGGACTTTATGACATCGAGGGAGCTGGAGTGG 210
 Qy 1144 GAGAACATCGCAGGAGAAGCCCTTCACCCGGAGGAGCAGTACTCTAAG 1143
 Db 1084 ATGAAAGAGGTGACCTGAGGCGATGAGGACTGTGAGACTGAGTCAC 1087
 Db 1024 AGGCGGTGAGCTGTCCTTCAGCATCGTCCTGTGCAACACACTCACTGCTCCCTG 1083
 Qy 1088 GAGGACATCGCAGGAGAAGCCCTACCCAGGAGGAGCAGGACTGTGAGTCAC 1147
 Db 1144 GAGAACATCGCAGGAGAAGCCCTTCACCCGGAGGAGCAGTACTCTAAG 1203
 Qy 1208 CTTTGTGACCGAGCTAGCACACAGCAGCCCGCGCTGCGGGAGGAGCAGTACTCTAAG 1207
 Db 1148 GCTGACCTGAGTGCCTCCAGGAGAGACCTGAGGAGCTGAGTCAC 1143
 Db 1204 GCCGAGCTGAGTGCCTGAGGAGAGACCTGAGGAGCTGAGTCAC 1143
 Db 1144 GAGAACATCGCAGGAGAAGCCCTTCACCCGGAGGAGCAGTACTCTAAG 1203
 Qy 1260 AGAGATGGCCAAAGAAATTAGAACAGCTGGAGGAGCCCTGGAGCTG 1319
 Db 1321 AGAGAGGTCTCGAGGACTCTGAGACTT - - - - - CCGAGACCTGGAGTGCAG 1259
 Db 1261 CTCGGAGGACCTGCTGAGCATCGAGTCAGGATCCAGAACATTCGAGCA 1320
 Qy 1320 TGGCTGTTCTGTGAGGAGCTCAGCATCCAAAGCTTAAATTCTCCATAAATG 1379
 Db 1369 TGGCTGTTCTGTGAGGAGCTCAGCATCCAAAGCTTAAATTCTCCATAAATG 1428
 Db 1380 GGCTTCTCTGTGAGCATCTCAGAGTCTGGGGGGAGCTGAGCTGAGTCAC 1439
 Qy 1429 GGCTTCTCTGTGAGCATCTCAGAGTCTGGGGGGAGCTGAGTCAC 1487
 Db 1440 TATAAGGA - - - - - CATCTCATCATCCGGGGTAAGAGTCAGTAAGGGAGCCT 1491
 Qy 1488 TCTCAGGAGTACCTTTTTAACACAGGTTAACAGTCAGATTAGCAGCTT 1547
 Db 1492 CTTCACAG 1499
 Qy 1548 CCTCACAG 1555
 Db 511 ATCTCTGATGGGGTGAATTCACACAAAGAAATGCTCACTTGTGACCA 570
 Qy 428 ATCCCTGATGGGGTGAATCCTCACACAAAGAAATGCTCACTTGTGACCA 487
 Db 488 GAAACATTTGTTGTTGAGACAGATATCCACACATCAACTGTGACCTT 547
 Qy 571 GAAACATCACTGTTGAGACAGATATCCACACATCAACTGTGACCTT 630
 Db 548 GGTCTGGCTCAGGAAATAGAGATGGATGTTGAGATTAGAATTTGGAGCCGGAA 607
 Db 631 GCGCTGGCTCAGGAAATAGAGATGGAGTCAATTAAACATTTGGACACTGAA 690
 Qy 608 TTGTTGCTCCGAGAATGCAACTAGCAGGCCCTGGGTCTGGCTGAGCTGGAGC 667
 Db 691 TTGTTGCTCCGAGAATGCAACTAGCAGGCCCTGGGTCTGGCTGAGCTGGAGC 746
 Qy 668 ATAGGGCTCATCACCTAACCTCTTAAGGGAGATCCCTTCTCTGAGGAGCAG 727
 Db 747 - - - - - TCTAGTGGAGCTCCCTCTGGAGACAA 733
 Qy 728 CGGAAACACTGCAATATCACATCGTGGAGTCACTTGTGAGGATCTCAGC 787
 Db 784 CGAGAACCTGCAATATCACCTGCTGAGCTTGTGAGGATCTCAGC 843
 Qy 788 CATAGCAGGAGCTGGCCAAAGAACCTTGTGAGGAGCTTGTGAGGAGCCGAA 847

RESULT 12
 US-09-649-163-7647
 : Sequence 7647, Application US/09649163
 ; GENERAL INFORMATION:
 ; APPLICANT: Holtzman, Douglas A.
 ; APPLICANT: Galvin, Katherine A.
 ; APPLICANT: Leib, Kevin R.
 ; APPLICANT: Kingsbury, Gillian A.
 ; APPLICANT: Weich, Nadine S.
 ; APPLICANT: McCarthy, Sean A.
 ; APPLICANT: Williamson, Mark A.
 ; APPLICANT: Richardson, Jennifer A.
 ; APPLICANT: MacBeth, Kyle J.
 ; APPLICANT: Fraser, Christopher C.
 ; APPLICANT: Villeneuve, Jean-Duc M. G.
 ; APPLICANT: Goodarl, Andrew D.J.
 ; APPLICANT: Silos Santiago, Inmaculada
 ; APPLICANT: White, David
 ; APPLICANT: Pan, Yang
 ; APPLICANT: Busfield, Samantha J.
 ; APPLICANT: Deeds, James

APPLICANT: Lee, John
 APPLICANT: Shyuan, Andrew W.
 TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
 FILE REFERENCE: 1600-1161-001
 CURRENT APPLICATION NUMBER: US/09/649,163
 PRIOR APPLICATION NUMBER: 60/150,608
 PRIOR FILING DATE: 1999-08-25
 NUMBER OF SEQ ID NOS: 10535
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 7647
 LENGTH: 1512
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE: misc_feature
 NAME/KEY: misc_feature
 LOCATION: (1)..(1512)
 ; OTHER INFORMATION: n = A,T,C or G
 ; US-09-649-163-7647

Query Match 58.5%; Score 1019.2; DB 25; length 1512;
 Best Local Similarity 99.1%; Pred. No. 1.2e-239;
 Matches 1045; Conservative 0; Mismatches 8; Indels 2; Gaps 2;

Qy 687 TCCTCTTAAGTGGGCATCCCTTCTGGAGACAGAACACTGGCAATA 746
 Db 301 TCACCTTAAGTGGGCATCCCTTCTGGAGACAGAACACTGGCAATA 360
 Qy 747 TCACATCAGTGAGTTACGACTTGTATGAGGAATTCTTCAGCCATACGAGCGAGCTGGCCA 806
 Db 361 TCAGAGCAGTGAGTTACGACTTGTATGAGGAATTCTTCAGCCAGACGAGCGAGCTGGCCA 420
 Qy 807 AGGCTTTATCGSAGCTCTGGTTAAAGAGAACGCCGAAACGCTCTAACATCAAAGGG 866
 Db 421 AGGACTTTATCGSAGCTCTGGTTAAAGAGAACGCCGAAACGCTCTAACATCAAAGGG 479
 Qy 867 CTCTCAGACACCCCTGGATCACGGGGACACAGAACGGCATGGTG-CGAGGGAG 925
 Db 480 CTCTCAGACACCCCTGGATCACGGGGACACAGAACGGCATGGTGCGAGGGAG 539
 Qy 926 TCTCTGGTCAATCTGGAGACTTCAGGAAGCAGTAGTGTGCGAGGGTGGAAGCTTRCC 985
 Db 540 TCTCTGGTCAATCTGGAGACTTCAGGAAGCAGTAGTGTGCGAGGGTGGAAGCTTRCC 599
 Qy 986 TTCAGCATCTGGCTCTGGCAACACCTCACCGCTCTCTGAGAAGAGGGCCTACCTG 1045
 Db 600 TTCTCGCATCTGGCTCTGGCAACACCTCACCGCTCTCTGAGAAGAGGGCCTACCTG 659
 Qy 1046 AGGGCGGATGAGGACTGTGAGGAGTGTGAGAGTGACACTGGGGACATCGCAGGG 1105
 Db 650 AGGGGGATGAGGGCTGTGAGGAACCTGTGAGGAGACTGGGGACATCGCAGGG 719
 Qy 1105 AAACGCTTCACCCACGGAGGGAGAGACCTCTTAAGTGGCTGACTCGCTGTGAC 1165
 Db 720 AAACGCTTCACCCACGGAGGGAGAGACCTCTTAAGTGGCTGACTCGCTGTGAC 779
 Qy 1165 GCGGGGGGGTCTGGCCAGCGGGCTCTTGTGAGACTTTGACCCGGCTCG 1225
 Db 780 GCGGGGGGGTCTGGCCAGCGGGCTCTTGTGAGACTTTGACCCGGCTCG 839
 Qy 1226 CACCAAGACCCGGGGCTCTGAGGAGATGGGCCAAGGAATTAGAG 1285
 Db 840 CACCAAGACCCGGGGCTCTGAGGAGACTTTGACCCGGCTCG 899
 Qy 1286 AGCTTGAGGCAACCGAGGACCTGGGGAGCTCTGGCTGACTCGCTGTGAGGGCTCG 1345
 Db 900 AGCTTGAGGCAACCGAGGACCTGGGGAGCTCTGGCTGACTCGCTGTGAGGGCTCG 959
 Qy 1346 AGCTTGAGGCAACCGAGGACCTGGGGAGCTCTGGCTGACTCGCTGTGAGGGCTCG 1405
 Db 960 AGCTTGAGGCAACCGAGGACCTGGGGAGCTCTGGCTGACTCGCTGTGAGGGCTCG 1019

Qy 1405 AGCTGGGGGGGAGCTGCGACTTAGGAACAACTATTAAGGACATCTCATCATCGG 1465
 Db 1020 AGCTGGGGGGAGCTGCGACTTAGGAACAACTATTAAGGACATCTCATCATCGG 1079
 Qy 1466 GGTCAGGTTAGGACTAAGGCGCTCTCCACAGGCTCAGGGCTCAGAACAGCGCTGG 1525
 Db 1080 GGTCAGGTTAGGACTAAGGCGCTCTCCACAGGCTCAGGGCTCAGAACAGCGCTGG 1139
 Qy 1526 CCAAATTAACAGAGAGACAGAGCTCTCCATGGAAACAGGGGATGGAGAAG 1585
 Db 1140 CCAAATTAACAGAGAGACAGAGCTCTCCATGGAAACAGGGGATGGAGAAG 1199
 Qy 1586 TGAACCTTGGTGTGGAGGACCATCTGTGACTCTCCAGACCATGAGCCAGGGT 1645
 Db 1200 TGAACCTTGGTGTGGAGGACCATCTCCAGAACATGGAGAAGCCAGGGT 1259
 Qy 1646 CAGGTGACCAACACCTGAGACCTCTGACCTCTGAGAAGGCCCATTGCTGGCCGCGCATGTGAA 1705
 Db 1260 CAGGTGACCAACACCTGAGACCTCTGACCTCTGAGAAGGCCCATTGCTGGCCGCGCATGTGAA 1319
 Qy 1706 TTTCGCTCATTTTATTAACTCTGTGTTACCTG 1741
 Db 1320 TTTCGCTCATTTTATTAACTCTGTGTTACCTG 1355

RESULT 13
 ; Sequence 802, Application US/09652816
 ; GENERAL INFORMATION:
 ; APPLICANT: Gutierrez-Ramos, Jose-Carlos
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
 ; FILE REFERENCE: THEREFOR
 ; CURRENT APPLICATION NUMBER: US/09/652,816
 ; CURRENT FILING DATE: 2000-08-31
 ; PRIOR APPLICATION NUMBER: 60/152,111
 ; PRIOR FILING DATE: 1999-08-31
 ; NUMBER OF SEQ ID NOS: 9647
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 8022
 ; LENGTH: 1512
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(1512)
 ; OTHER INFORMATION: n = A,T,C or G
 ; US-09-652-816-8022

Query Match 58.5%; Score 1019.2; DB 25; Length 1512;
 Best Local Similarity 99.1%; Pred. No. 1.2e-239;
 Matches 1046; Conservative 0; Mismatches 8; Indels 2; Gaps 2;

Qy 687 TCCTCTTAAGTGGGCATCCCTTCTGGAGACAGAACACTGGCAATA 746
 Db 301 TCACCTTAAGTGGGCATCCCTTCTGGAGACAGAACACTGGCAATA 360
 Qy 747 TCACATCAGTGAGTTACGACTTGTATGAGGAATTCTTCAGCCATACGAGCGAGCTGGCCA 806
 Db 361 TCAGAGCAGTGAGTTACGACTTGTATGAGGAATTCTTCAGCCAGACGAGCGAGCTGGCCA 420
 Qy 807 AGGCTTTATCGSAGCTCTGGTTAAAGAGAACGCCGAAACGCTCTAACATCAAAGGG 866
 Db 421 AGGACTTTATCGSAGCTCTGGTTAAAGAGAACGCCGAAACGCTCTAACATCAAAGGG 479
 Qy 867 CTCTCAGACACCCCTGGATCACGGGGACACAGAACGGCATGGCTCG 925
 Db 480 CTCTCAGACACCCCTGGATCACGGGGACACAGAACGGCATGGCTCG 539
 Qy 926 TCTCTGGTCAATCTGGAGACTTCAGGAGACATGTTGACCCGGCTCG 985
 Db 540 TCTCTGGTCAATCTGGAGACTTCAGGAGACATGTTGACCCGGCTCG 599

QY 986 TTCAAGCATCGTCTCTGTCACACCACTCACCGCTCGTGAAGAAGGTCACCTG 1045 ; LOCATION: (1)..(1512)
; OTHER INFORMATION: n = A,T,C or G
; US-09-652-913-8169
Db 600 TTCAAGCATCGTCTCTGTCACACCACTCACCGCTCGTGAAGAAGGTCACCTG 659
; Query Match 58.5%; Score 1019.2; DB 25; Length 1512;
; Best Local Similarity 99.1%; Pred. No. 1.2e-239; 8; Index 2; Gaps 2;
; Matches 1046; Conservative 0; Mismatches 8;
; Db 660 AGGGCGGATGAGGAACCTGAGGAACCTGAGAGATGAGAGTCACCTGAGGG 719
; Db 1046 AAAAGCGCTCCACCCACGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1105
; Db 720 AAAGCCTCCACCCACGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 779
; Db 1166 GCGCAGGAGGTTGGCCACGGCGCTCCCTTGCGAGACTTTGGACCCAGCTCAG 1225
; Db 780 GCGCAGGAGGAGGTTGGCCACGGCGCTCCCTTGCGAGACTTTGGACCCAGCTCAG 839
; Db 1226 CACACGACCGGGCTCTGAGCCTTGCAAAAGAGATGGGCCAAGGAATTCAGAG 1285
; Db 840 CACACGACCGGGCTCTGAGCCTTGCAAAAGAGATGGGCCAAGGAATTCAGAG 899
; Db 1286 AGCTTGAGGAGGAGGAGGACCTGGAGCTTGCGTCTCTGAGGAGCTTGACGCC 1345
; Db 900 AGCTTGAGGAGGAGGAGGACCTGGAGCTTGCGTCTCTGAGGAGCTTGACGCC 959
; Db 1346 AGCATTCCAAAGCTCTTAATTCCTCCATAAAATGGCTTCTGTCCTCCATCTCAG 1405
; Db 960 AGCATTCCAAAGCTCTTAATTCCTCCATAAAATGGCTTCTGTCCTCCATCTCAG 1019
; Db 1406 ACTCTGGTGGAGGAGCTTGCGTCTCTGAGGAGCTTGAGAACATAAAGGACATCCTCATCACGG 1465
; Db 1020 ACTCTGGTGGAGGAGCTTGCGTCTCTGAGGAGCTTGAGAACATAAAGGACATCCTCATCACGG 1079
; Db 1466 GTGAGGTAGAGTAGGCAGCTTCTCACAGGCTGAGGGGTCAAGACCCGCTGG 1525
; Qy 1466 GTGAGGTAGAGTAGGCAGCTTCTCACAGGCTGAGGGGTCAAGACCCGCTGG 1525
; Db 1080 GTCTGAAGGTCACTAAAGGACGCTCTCTCAGGCTGAGGGGTCAAGACCCGCTGG 1139
; Qy 1526 CCAAAATTACCCACAGAGAAGGAGCTCTCCATGGGACACGGTGTGGGAAC 1555
; Db 1140 CCAAAATTACCCACAGAGAAGGAGCTCTCCATGGGACACGGTGTGGGAAC 1199
; Qy 1586 TGAACCTGGGTGTGGGACCATCTGTGACCTCCACGGACAGCATGGAACCCGGACGT 1645
; Db 1200 TGAACCTGGGTGTGGGACCATCTGTGACCTCCACGGACAGCATGGAACCCGGACGT 1259
; Qy 1646 CAGGCTTACCAACCCCTGAGCTCTGAGAGGAGGAGGAGGAGGAGGAGGAGG 1705
; Db 1260 CAGGCTTACCAACCCCTGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1319
; Qy 1706 TTTCGCTCATTAACTCTGGTTACCTGA 1741
; Db 1320 TTTCGCTCATTAACTCTGGTTACCTGA 1355
; RESULT 14
; US-09-652-913-8169
; Sequence 8169, Application US/09652913
; GENERAL INFORMATION:
; APPLICANT: Faib, Dean R.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600-1174-001
; CURRENT APPLICATION NUMBER: US/09/652, 913
; PRIOR APPLICATION NUMBER: 2000-08-31
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 10833
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 8169
; LENGTH: 1512
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: NAME/KEY: misc_feature

RESULT 15
 US-09-652-917-2793
 ; Sequence 2793, Application US/09652917
 ; GENERAL INFORMATION:
 ; APPLICANT: Shylian, Andrew W.
 ; APPLICANT: Holtzman, Douglas A.
 ; APPLICANT: Di Stefano, Peter
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
 ; FILE REFERENCE: 1600-1170-001
 ; CURRENT APPLICATION NUMBER: US/09/652,917
 ; CURRENT FILING DATE: 2000-08-30
 ; PRIOR APPLICATION NUMBER: 60/151,422
 ; PRIOR FILING DATE: 1999-08-30
 ; NUMBER OF SEQ ID NOS: 3855
 ; SOFTWARE: FastBQ for Windows Version 4.0
 ; SEQ ID NO: 2793
 ; LENGTH: 1512
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc. feature
 ; LOCATION: (1)..(1512)
 ; OTHER INFORMATION: n = A,T,C or G
 ; US-09-652-917-2793

Query Match 58 5%; Score 1019.2; DB 25; Length 1512;
 Best Local Similarity 99.1%; Pred. No. 1.2e-239;
 Matches 1046; Conservative 0; Mismatches 8; Indels 2; Gaps 2;

Qy 687 TCCCTTAATGGGATCCCTTCTGGAGACAGAGACAGAGACAACTGGAAATA 746
 Db 301 TCAACTAAGTGGGACATCCCTTCTGGAGACAGAGACAACTGGAAATA 360

Qy 747 TCAATCAGTGGTACGACTTCTGGAGATCTTCAGCCATACGAGGAGCTGGCCA 806
 Db 361 TCAAGCAGTGAGTACGACTTCTGGAGATCTTCAGCCAGCAGGAGCTGGCCA 420

Qy 807 AGGCTTATTGGAGCTCTGGTAAGAGAGACCCGAAACGGCTCAGATCCAGGG 866
 Db 421 AGGCTTATTGGAGCTCTGGTAAGAGAGACCCGAAACGGCTCAGATCCAGGG 479

Qy 867 CTCTCAGACACCCCTGGATCACGCCGGTGACAAACCGAGAGCCATGGG-CGAGGGGG 925
 Db 480 CTCTCAGACACCCCTGGATCACGCCGGTGACAAACCGAGAGCCATGGGCGGAGGG 539

Qy 926 TCTGTGGTCAATCTGGAGACTTCTGGAGCTGGAGAGCTTCC 985
 Db 540 TCTGTGGTCAATCTGGAGACTTCTGGAGCTGGAGAGCTTCC 599

Qy 986 TTCTGCACTGTGTCCTGGCAACCACTCACCGCTCTGTAGAGAGGTCACCTG 1045
 Db 600 TTCTGCACTGTGTCCTGGCAACCACTCACCGCTCTGTAGAGAGGTCACCTG 659

Qy 1046 AGGCCGGATGAGGAGCTGGAGATCTGGAGAGCTGGAGAGCTTCC 985
 Db 650 AGGCCGGATGAGGAGCTGGAGAGCTTCC 719

Qy 1106 AAACGCTTCACCCAGGGAGGAGGAGCTGGAGAGCTTCC 1165
 Db 720 AAGGCCCTTCACCCAGGGAGGAGGAGCTTCC 779

Qy 1166 GCCGGGAGGTTGGCCAGGAGCTTGTGAGAGCTTGTGAGAGCTTGTGAGAGCTGAG 1225
 Db 780 GCCAGGAGGCTGGCCAGGGAGCTTGTGAGAGCTTGTGAGAGCTGAGCTGAG 839

Qy 1226 CACCGACCCGGGGTCTGGAGCTTGTGAGAGATGGCCAAAGAATCAGAG 1285
 Db 840 CACCGACCCGGGGTCTGGAGCTTGTGAGAGATGGCCAAAGAATCAGAG 899

Qy 1286 AGCTTGAGGCAACCGAGACCCCTGGAGAGCTGGAGCTGGCTCTGTGAGGGGCTCC 1245
 Db 900 AGCTTGAGGCAACGGAGACCCCTGGGGCTGTGGCTCTGTGAGGGGCTCC 959

Qy 1346 AGCATCCCAAAAGCTTCAATTCATCAAAATGGGTTTCCCTGTGAGCCATCTCG 1405
 Db 960 AGCATCCCAAAAGCTTCAATTCATCAAAATGGGTTTCCCTGTGAGCCATCTCG 1019

Qy 1406 AGTCGGGGGGAGTGGACTTAGGAAACAAATAAGGACATCCATCATCACGG 1465
 Db 1020 AGTCGGGGGGAGTGGACTTAGGAAACAAATAAGGACATCCATCATCACGG 1079

Qy 1466 GGTGAGGGTCAAGTAAAGCCGGCTCTTCAAGGTGAGGGGGTCAAGAACCCGCTCG 1525
 Db 1080 GGTGAGGGTCAAGTAAAGCCGGCTCTTCAAGGTGAGGGGGTCAAGAACCCGCTCG 1139

Qy 1525 CCAAATAATPACACAGAGAGCAGTCTCCCATGGAAAGGGGTGAGGAAG 1585
 Db 1140 CCAAATAATPACACAGAGAGCAGTCTCCCATGGAAAGGGGTGAGGAAG 1199

Qy 1586 TGAACCTGGGTGAGGGCCAACTCTGACCTCCAGAACATGGAGCCAGGCT 1645
 Db 1200 TGAACCTGGGTGAGGGCCAACTCTGACCTCCAGAACATGGAGCCAGGCT 1259

Qy 1646 CAGCTGACCAACCTCGAACCTCTGGAGACGCCATTTGAGGGCCAGTGTGA 1705
 Db 1260 CAGGTGACCAACCTCGAACCTCTGGAGACGCCATTTGAGGGGTGAGGAAG 1319

Qy 1705 TTGTGTCATTTTATTAACCTCTGGTTTACCTGA 1741
 Db 1320 TTGTGTCATTTTATTAACCTCTGGTTTACCTGA 1355

Search completed: April 4, 2003, 22:30:05
 Job time : 5391.24 secs

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Om nucleic - nucleic search, using sw model

Run on:

April 4, 2003, 20:49:32 ; Search time 941.167 Seconds

(without alignments) 7198.356 Million cell updates/sec

Title: US-09-719-748-1

Perfect score: 1742

Sequence: 1 gaccggggcagtcggctc.....aaacttctgtgttacctgaa 1742

Scoring table: IDENTITY_NUC GpOp 10.0 , Gapext 1.0

Searched: 5575038 seqs, 1944561127 residues

Total number of hits satisfying chosen parameters: 11150076

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%*

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents Na New:*

1: /cgn2_6/podata/2/pna/pct_new comb.seq:*

2: /cgn2_6/podata/2/pna/us06_new_comb.seq:*

3: /cgn2_6/podata/2/pna/us07_new_comb.seq:*

4: /cgn2_6/podata/2/pna/us08_new_comb.seq:*

5: /cgn2_6/podata/2/pna/us09_new_comb.seq:*

6: /cgn2_6/podata/2/pna/us10_new_comb.seq:*

7: /cgn2_6/podata/2/pna/us11_new_comb.seq:*

8: /cgn2_6/podata/2/pna/us12_new_comb.seq:*

9: /cgn2_6/podata/2/pna/us60_new_comb.seq:*

Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1727.4	99.2	2085	9 US-60-443-566-647
c	2 1199.8	68.9	1442	6 US-09-724-676-34736
c	3 1199.8	68.9	1442	6 US-09-724-676-34736
c	4 1032.4	59.3	1732	8 US-10-144-771-3361
c	5 52.4	30.7	601	5 US-09-947-071-15358
c	6 517.2	29.7	2157	5 US-09-949-16-1966
c	7 517.2	29.7	2201	9 US-09-443-566-467
c	8 515.6	29.6	2105	5 US-09-949-016-195
c	9 515.6	29.6	2132	1 PCT-US02-31357-118
c	10 515.6	29.6	2132	8 US-10-262-445-118
c	11 515.4	29.6	2570	6 US-09-724-676-20895
c	12 515.4	29.6	2570	6 US-09-724-676-20895
c	13 514.6	29.5	979	6 US-09-724-676-20893
c	14 514.6	29.5	979	6 US-09-724-676-20893
c	15 513.8	29.5	1410	8 US-10-144-771-9285
c	16 512.4	29.4	5526	8 US-10-144-771-888
c	17 512.4	28.7	1514	1 PCT-US03-0482-3594
c	18 499.4	28.7	1514	1 PCT-US03-0194-3489
c	19 499.4	28.7	8	US-10-338-044-2139
c	20 499.4	28.7	1514	9 US-10-436-643-3489
c	21 495.4	28.4	6074	9 US-60-443-566-691
c	22 494.6	28.4	5910	1 PCT-US03-02484-97
c	23 494.6	28.4	5910	6 US-09-949-016-2021
c	24 494.6	28.4	5910	8 US-10-133-937-12

ALIGNMENTS

RESULT 1
US-60-443-566-647
; Sequence 647, Appli
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; ATTORNEY: BEGOVITCH, Ann
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001447
; CURRENT FILING DATE: 2003-01-30
; NUMBER OF SEQ ID NOS: 2502
; SEQ ID NO: 647
; LENGTH: 2085
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-60-443-566-647

Query Match 99.2%; Score 1727.4; DB 9; length 2085;
Best Local Similarity 99.3%; Pred. No. 0; Pred. No. 0;
Matches 1728; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 GACCGGGGAGCTGAGCTCCGGCGATGTTGATGTCAGGCCCTAACAGGAGTCAA 60
Db 8 GACCGGGGAGCTGAGCTCCGGCGATGTTGATGTCAGGCCCTAACAGGAGTCAA 67

QY 61 CATGGAGCCATTCAAGCAGCAGAGGTGGAGGACTTTATGACATCGGAGAGGAGCTGG 120
Db 68 CATGGAGCCATTCAAGCAGCAGAGGTGGAGGACTTTATGACATCGGAGAGGAGCTGG 127

QY 121 GAGTGGCCAGTTGCCATCTGAGAAGCTGCCGGAGAGGAGCAGCGGGCTTGAGTATGC 180
Db 128 GAGTGGCCAGTTGCCATCTGAGAAGCTGCCGGAGAGGAGCAGCGGGCTTGAGTATGC 187

QY 181 AGCCAGTCTCATAGAAGCGGAGCGGGGAGCCAGCGGGGTGAGGCCGGAGGA 240
Db 188 AGCCAGTCTCATAGAAGCGGAGCGGGTGTGAGGCCGGAGGA 247

QY 241 GATGGAGCGGGAGGTGGACATCCGGCGAGGAGCTGTCACAGCTCA 300
Db 248 GATGGAGCGGGAGGTGGACATCCGGCGAGGAGCTGTCACAGCTCA 307

QY 301 CGAGCTCTATGACACCCACCGCTGACATCTTGAGCTAGTGTCTGGAGGA 360
Db 308 CGAGCTCTATGACACCCACCGCTGACATCTTGAGCTAGTGTCTGGAGGA 367

QY	361	GCTCTTGGATTCTGGGCCAGAGGGTCACTGAGTGAGGGAGCCACAGTCAT	420	Db	1448	ATAAAGACATCCTCATCATCACGGGGTGAAGGTGACTNAGGCCCTCTCACAGG	1507
Db	368	GCTCTTGGATTCTGGGCCAGAGGGTCACTGAGTGAGGGAGCCACAGTCAT	427	QY	1501	CTGAGGGGGTCAAGAACCCAGCCTGGCAAMATTACCAAGAGAGCAGAGTCCTCCCA	1560
QY	421	TAGCAGATCTCTGATGCGGTAATCTCACACAAAGAAATTCGACTTGTGATC	480	Db	1508	CTGAGGGGGTCAAGAACCCAGCCTGGCAAMATTACCAAGAGAGCAGAGTCCTCCCA	1567
Db	428	TAGCAGATCTCTGATGCGGTAATCTCACACAAAGAAATTCGACTTGTGATC	487	QY	1561	TGGGGACAGGGTGTAGGAAAGTGACCTTGGTGTAGGGAGACAACTCTGACT	1620
QY	481	CAAGCCGAAACATATTGTTGAGACAGAAATTCGATCCACAAAGAAATTCGACTTGTGATC	540	Db	1568	TGGGGACAGGGTGTAGGAAAGTGACCTTGGTGTAGGGAGACAACTCTGACT	1627
Db	488	CAAGCCGAAACATATTGTTGAGACAGAAATTCGATCCACAAAGAAATTCGACTTGTGATC	547	QY	1621	CCGAGACCATGAAACCCAGGAGTCAGGTGAGCCACCCACCTGGCAAAATTACCAAGAGAGCAGAGTCCTCCCA	1680
QY	541	TGACTTGTCTGCTCAGAAATGAGAAATGAGAAATGAGAAATGGGATGTTGAGAC	600	Db	1628	CCCAGAACATGGAAACCCAGGAGTCAGGTGAGCCACCCACCTGGCAAAATTACCAAGAGAGCAGAGTCCTCCCA	1687
Db	548	TGACTTGTCTGCTCAGAAATGAGAAATGAGAAATGGGATGTTGAGAC	607	QY	1681	CGATTGTGGCCGCTGTGTAAATTGCTCATTTTAACTCTGTTACCTG	1740
QY	601	GCGGAATTGTTGCTCAGAAATGAGAAATGAGAAATGGGATGTTGAGAC	660	Db	1688	CCATTGCTGGCCGCACTGTTAATTGCTCATTTTAACTCTGTTACCTG	1747
Db	608	GCGGAATTGTTGCTCAGAAATGAGAAATGGGATGTTGAGAC	667	QY	1741	A 1741	
QY	661	GTGGAGCATGGGTCATCCTCATCTAGTGGAGCATCCCTTCTGGAGA	720	Db	1748	A 1748	
Db	668	GTGGAGCATGGGTCATCCTCATCTAGTGGAGCATCCCTTCTGGAGA	727				
QY	721	CACCGAGCTTGGCAACTGCAAAATTCGATCATCGTGTGAGTTACCTTGATGAGGAAT	780				
Db	728	CACGAGCGAAACTGCAAAATTCGATCATCGTGTGAGTTACCTTGATGAGGAAT	787				
QY	781	CTTCAGCCATAGCGGAGTGGCAAGACTTATTGAGCTTGTAAAGAGAC	840				
Db	788	CTTCAGCCATAGCGGAGTGGCAAGACTTATTGAGCTTGTAAAGAGAC	847				
QY	841	CCGGAACGGCTCACATCCAGAGGCTCTAGACACCCCTGGTACCCGGTGCACAA	900				
Db	848	YCGGAACGGCTCACATCCAGAGGCTCTAGACACCCCTGGTACCCGGTGCACAA	907				
QY	901	CCAGCAAGCCATGGTGCAGCGAGGTGTGTCAATCTGGAGAACTTCAGGAGGATA	960				
Db	908	CCAGCAAGCCATGGTGCAGCGAGGTGTGTCAATCTGGAGAACTTCAGGAGATA	967				
QY	961	TGTCCCGAGGGTGTGAGCTTCTTCAGATCGTGTCCCTGTGCAACACCTACCCG	1020				
Db	968	TGTCCCGAGGGTGTGAGCTTCTTCAGATCGTGTCCCTGTGCAACACCTACCCG	1027				
QY	1021	CTCGCTGTGAGAGCTGCACTGGCCGAATGAGCTTGTGAGGTGA	1080				
Db	1028	CTCGCTGTGAGAGCTGCACTGGCCGAATGAGCTTGTGAGGTGA	1087				
QY	1081	CACTGAGGAGCATCCAGGAGGAAGCCCTCCACCATGGAGGAGGAGCAGACCTC	1140				
Db	1088	CACTGAGGAGCATCCAGGAGGAAGCCCTCCACCATGGAGGAGCAGACCTC	1147				
QY	1141	CTRACTGGCTGACTGAGTGAGTGAGGAGGTTGGGCCAGGGGGCTCCCT	1200				
Db	1148	CTRACTGGCTGACTGAGTGAGGAGGTTGGGCCAGGGGGCTCCCT	1207				
QY	1201	GTGCGAGCTTGTGAGACAGCTGAGACCCGGCTCTGAGACTTGCGAGA	1260				
Db	1208	GTGCGAGCTTGTGAGACCCGGCTCTGAGACTTGCGAGA	1267				
QY	1261	GAGATGCCCAAGGAATTCAGAGAGCTTGCGAGGAGGAGCTGGAGCTG	1320				
Db	1268	GAGATGCCCAAGGAATTCAGAGAGCTTGCGAGGAGCTGGAGCTG	1327				
QY	1321	GGCTGTCTCTGTGAGGAGGCTCAGATCCAACTCTTAATTCCTCATTAATGG	1380				
Db	1328	GGCTGTCTCTGTGAGGAGGCTCAGATCCAACTCTTAATTCCTCATTAATGG	1387				
QY	1381	GCTTGTCTCTGTGAGGAGGCTCAGATCCAACTCTTAATTCCTCATTAATGG	1440				
Db	1388	GCTTGTCTCTGTGAGGAGGCTCAGATCCAACTCTTAATTCCTCATTAATGG	1447				
QY	1441	ATAAGGAAATCCCTCATCATCACCGGGTCAAGTCAAGGCAGCTCTCACGG	1500				

Query Match						
Best Local Similarity		Score		DB		Length
Qy	421	TAAGCAGATCCTGAGTGGGTGACTACCTTCACACAGAAATTGCACTTGACT	480			
Db	1015	TAAGCAGATCCTGAGTGGGTGACTACCTTCACACAGAAATTGCACTTGACT	956			
Qy	481	CAAGCCAGAAACCTTATGTTGAGACAGAAATTCCATTCAACATCAGCTAT	540			
Db	955	CAAGCCAGAAACCTTATGTTGAGACAGAAATTCCATTCAACATCAGCTAT	896			
Qy	541	TGACTTGTCTGCTCAGGAATAGAAGATGGGTTGATTAGAAATTGGAC	600			
Db	895	TGACTTGTCTGCTCAGGAATAGAAGATGGGTTGATTAGAAATTGGAC	836			
Qy	601	GCGGGAATTGTTCTCCAGAAATTGAGAAATTCCATTCAACATCAGCTAT	660			
Db	835	GCGGGAATTGTTCTCCAGAAATTGAGAAATTCCATTCAACATCAGCTAT	776			
Qy	661	GTGGAGCATAGGCCATACCTTCAGAAATTGAGAAATTGGGTTGAGAAT	720			
Db	775	GTGGAGCATAGGCCATACCTTCAGAAATTGAGAAATTGGGTTGAGAAT	716			
Qy	721	CACCAAGCAGAAACCTGGCAATTCAGGAAATTGAGAAATTGGGTTGAGAAT	780			
Db	715	CACCAAGCAGAAACCTGGCAATTCAGGAAATTGGGTTGAGAAT	656			
Qy	781	CTTCAGCCATACGGGAGCTGCGCAAGGACTTATTGGAAACTCTCGGTAAAGAC	840			
Db	655	CTTCAGCCATACGGGAGCTGCGCAAGGACTTATTGGAAACTCTCGGTAAAGAC	596			
Qy	841	CCGGAAACGGCTCAATCAAGGGCTTCAGAACCCCTGGTACAGGAGGAA	900			
Db	595	CCGGAAACGGCTCAATCAAGGGCTTCAGAACCCCTGGTACAGGAGGAA	536			
Qy	901	CCAGCAAGCCATGGTGGACGGGGTCTGGTAACTCTGAGAACTTGGAGAAT	960			
Db	535	CCAGCAAGCCATGGTGGACGGGGTCTGGTAACTCTGAGAACTTGGAGAAT	476			
Qy	961	TGTCGCGAGGGGGGGGAAGGCTTCTTCAGTCGGCCCTTGCAACCCCTACCG	1020			
Db	475	TGTCGCGAGGGGGGGGAAGGCTTCTTCAGTCGGCCCTTGCAACCCCTACCG	416			
Qy	1021	CTGGCTGATGAGAGGGCACCTGAGCCGGATGAGGACTCTGAGAGTGA	1080			
Db	415	CTGGCTGATGAGAGGGCACCTGAGCCGGATGAGGACTCTGAGAGTGA	356			
Qy	1081	CACTGAGGACATCGCAGGAGGAAGCCCTCACCACGGAGGAGCACCTC	1140			
Db	355	CACTGAGGAGACATCGCAGGAGGAAGCCCTCACCACGGAGGAGCACCTC	296			
Qy	1141	CTTACTGGCTGACTCGCTGGCCAGGGGTTGGCCACGGGGCTCCCT	1200			
Db	295	CTTACTGGCTGACTCGCTGGCCACGGGGCTCCCT	236			
Qy	1201	GTGGAGA 1207				
Db	235	GTGGAGA 229				
RESULT 3						
US-09-724-676A-34736/C						
; Sequence 34736, Application US/0924676A						
; GENERAL INFORMATION:						
; APPLICANT: Compugen LTD						
; TITLE OF INVENTION: Variants of alternative splicing						
; FILE REFERENCE: 129181.4 Compugen						
; CURRENT APPLICATION NUMBER: US/09/124,676A						
; CURRENT FILING DATE: 2000-11-28						
; NUMBER OF SEQ ID NOS: 97222						
; SOFTWARE: PatentIn version 3.2						
; LENGTH: 1442						
; SEQ ID NO: 34736						
; TYPE: DNA						
; ORGANISM: Homo sapiens						
; US-09-724-676A-34736						
Query Match						
Best Local Similarity		Score		DB		Length
Matches 1201;		99.5%;		Pred. No. 3.5e-296;		
; Conservative		2;		MisMatches		4;
; Indels		0;		Gaps		0;
; Gaps		0;		;		
Qy	1	GACCGCGGCCAGCTCAGCTCCCGCGATTGTTCCAGGCCCTCAATGAGGAGTCCAA	60			
Db	1435	GACCGGGGGAGCTCAGCCCTCCCGCGATTGTTCCAGGCCCTCAATGAGGAGTCCAA	1376			
Qy	61	CATGGAGCATTCAGCAGAGGGTGGAGGACTTTATGACATGGAGAGCTGGCTCG	120			
Db	1375	CATGGAGCATTCAGCAGAGGGTGGAGGACTTTATGACATGGAGAGCTGGCTCG	1316			
Qy	121	GAGTGGCCAGTTGCCATCTGGAGAGTGCCGGAGAGGAGCAGGGGCTTGAGTATGC	180			
Db	1315	GAGTGGCCAGTTGCCATCTGGAGAGTGCCGGAGAGGAGCAGGGGCTTGAGTATGC	1256			
Qy	181	AGCCAGTTCATAGAGGAGGCGAGGAGCTGGAGGAGCTTATGACATGGAGAGCTGG	240			
Db	1255	AGCCAGTTCATAGAGGAGGCGAGGAGCTGGAGGAGCTTATGACATGGAGAGCTGG	1196			
Qy	241	GATCGAGGGAGGGTGGAGCATCTGGCGAGGGTGGAGGAGCTTATGACATGGCTCA	300			
Db	1195	GATCGAGGGAGGGTGGAGCATCTGGCGAGGGTGGAGGAGCTTATGACATGGCTCA	1136			
Qy	301	CGAGCTCATGAGAACCCACCGAGGCTGACATCCTTGAGCTAGTCTGGAGGA	360			
Db	1135	CGAGCTCATGAGAACCCACCGAGGCTGACATCCTTGAGCTAGTCTGGAGGA	1076			
Qy	361	GCTCTTCGATTCCTGGCCAGAGGGACTCTGAGGAGGACTCTGAGGAGGAGGCCACCGCTCAT	420			
Db	1075	GCTCTTCGATTCCTGGCCAGAGGGACTCTGAGGAGGACTCTGAGGAGGAGGCCACCGCTCAT	1016			
Qy	421	TAAGCAGATCTGATGGGTAAGTACTCTCACACAGAAATTGCTCACACAGAAATTGCTCACACAGCTA	480			
Db	1015	TAAGCAGATCTGATGGGTAAGTACTCTCACACAGAAATTGCTCACACAGAAATTGCTCACACAGCTA	956			
Qy	481	CAAGCAGAACTATGTTGAGAACGAAATTCCATTCAACATCAAGCTAT	540			
Db	955	CAAGCAGAACTATGTTGAGAACGAAATTCCATTCAACATCAAGCTAT	896			
Qy	541	TGACTTGTCTGCTCAGAAATTGAGATGGAGCTTGAATTAAGATATTTGGAC	600			
Db	895	TGACTTGTCTGCTCAGAAATTGAGATGGAGCTTGAATTAAGATATTTGGAC	836			
Qy	601	GCCGGAAATTGTTGTTCTCAGAAATTGAGATGGAGCTTGAACGCCCTGGCTGGCTGGAGCTGACAT	660			
Db	835	GCCGGAAATTGTTGTTCTCAGAAATTGAGATGGAGCTTGAACGCCCTGGCTGGAGCTGACAT	776			
Qy	661	GTGGAGCATGGGCTCATCACCTACATCTTAACTGGAGCATCCCTTCTGGAGA	720			
Db	775	GTGGAGCATGGGCTCATCACCTACATCTTAACTGGAGCATCCCTTCTGGAGA	716			
Qy	721	CAGGAAGGAGAACCTGGCAATTCAGCAGACCTGGCAATTCAGCAGTGGAGGATT	780			
Db	715	CAGGAAGGAGAACCTGGCAATTCAGCAGACCTGGCAATTCAGCAGTGGAGGATT	656			
Qy	781	CITTCAGCCATAGAGGAGCTGCCAAGGATTATGGAGCTCTGGTTAAGAGAC	840			
Db	655	CITTCAGCCATAGAGGAGCTGCCAAGGATTATGGAGCTCTGGTTAAGAGAC	596			
Qy	841	CCGGAAACGGCTCACAACTCCAGAACGGCTCTAGACACCCCTGGATCAGGCCGTGGAGA	900			
Db	595	CCGGAAACGGCTCACAACTCCAGAACGGCTCTAGACACCCCTGGATCAGGCCGTGGAGA	536			
Qy	901	CCAGCAAGCCATGGTGGACGGGGTCTGGTAACTCTGAGAACTTGGAGAAT	960			
Db	535	CCAGCAAGCCATGGTGGACGGGGTCTGGTAACTCTGAGAACTTGGAGAAT	476			
Qy	961	TGTCGCGAGGGGGGGGAAGGCTTCTTCAGTCGGCCCTTGCAACCCCTACCG	1020			
Db	475	TGTCGCGAGGGGGGGGAAGGCTTCTTCAGTCGGCCCTTGCAACCCCTACCG	416			

RESULT 4
US-10-144-771-3361
Sequence 3361, Application US/10144771
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
; FILE REFERENCE: CI001321
; CURRENT APPLICATION NUMBER: US/10/144,771
; CURRENT FILING DATE: 2002-05-15
; NUMBER OF SEQ ID NOS: 47235
; SEQ ID NO 3361
; LENGTH: 1732
; TYPE: DNA
; ORGANISM: HUMAN
; US-10-144-771-3361

Query Match, Best Local Similarity 59.3%; Score 1032.4; DB 8; Length 1732;
Matches 1263; Conservative 83.8%; Pred. No. 2,3e-53; Mismatches 186; Indels 59; Gaps 6;

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QY 8 GCAGCTCAGCTCCGGCGGATGTTATGTCGGCTCAATGAGGGTCCAAACATGGAG 67
Db 91 GCAGCCGACGCTTCTGGCGATTTGATGTCGGCTCAATATGGAG 150
QY 68 CCAATTCAACAGGAGAAAGTGGGACTTATGACATGCGAGGAGCTGGAGTGGC 127
Db 151 ACGTTCAACAGGAGAAAGTGGGACTTATGACATGCGAGGAGCTGGAGTGGC 210
QY 128 CAGTTGGCCTCTGAAAGAGGAGTGGCGGGAGAACGGGCTTGGATGAGCGCAAG 187
Db 211 CAGTTGCCATCTGAAAGAGGAGTGGCGGGAGAACGGGCTTGGATGAGCGCAAG 270
QY 188 TTCTCAAGAAGCGAGGCCGGCGAGCCGGCGAGGCCGGCGAGGCCGGCGAGTGG 247
Db 271 TTCAATTAGAGGAGGAGGCCGGCGAGCCGGCGAGGCCGGCGAGGCCGGCGAGTGG 330
QY 248 CGGAGGGTAGCATCTGGGGAGTGTCTGCAACAAATGTCTACCTGCAGAGTC 307
Db 331 CGGGAGGTGGACATCTGGCGAGGTGCTGCACCCAAATCTCACCTGCAGAGTC 390
QY 308 TAGAGACCCGACGCTGTCACATCCTCTGAGTAGTGTCTGGAGGAGCTCTC 367
Db 391 TAGAGACCCGACGCTGTCACATCCTCTGAGTAGTGTCTGGAGGAGCTGTT 450
QY 428 ATCTGGATGGGTGACTACCTTCACACAGAATTCCTACTTGATCTCAAGCA 487
Db 511 ATCTGGATGGGTGAACTTCACACAGAATTCCTACTTGATCTCAAGCA 570
QY 488 GATTTCTGCCCCAGAGGACTCACTGAGGAGGCCGAGCTCATTAAGCAGTT 547
Db 451 GATTCCTGCCCCAGAGGACTGTTAAGGAGGCCACAGCTTAAAGCAGTT 610
QY 571 GAAACATCATCTTGTAGACAGAATTCACACACACAGCTGATGACTT 650

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RESULT 5
US-09-947-907-15358/C
Sequence 15358, Application US/09947907
; GENERAL INFORMATION:

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QY 548 GGTCTGGCTCAAGAAATGAAATGAGGACTGTGATTAGAATATTGGCGCGGAA 607
Db 631 GGCCTGGCTCAAGAAATGAGGACTGTGATTAAACATTTGGGACACCTGAA 690
QY 608 TTGTTGCTCGAGAAATGTAAGCTTGTGACTACAGCCCTGGCTCTGGAGGTGACATGGAGC 667
Db 691 TTGTTGCTCGAGAAATGTAAGCTTGTGACTACAGCCCTGGCTCTGGAGGTGACATGGAGC 746
QY 668 ATAGGCGTCATCACCTCTCTTAAGTGGAGCATCCCTTCCTGGAGCACAGA 727
Db 784 GAGAAACCTGGCAATATACAGCTGTTGAGTTACGACTTTGTGAGGATTTTCAGC 783
Db 747 - - - - - TCAACTGAGGCTCCCTCTGGAGCACAAA 843
QY 788 CATACGAGCGGCTGCCAAGGACTTATCGGAAGCTCTGGTAAGAGACCGGAA 847
Db 844 CAGACANGCGAGCTGGCAGAGCCTCATGGAGCTCTGGAGAATCTTCAG 903
QY 848 CGGTCTCAATCCAAGAGGCTCTAGACACCCCTGATAGCGCCGGACACAGAA 907
Db 904 CGCTTACATCCAAAGGAGCTCAGACACCTCTGATCGCGGTGACACCCGAA 963
QY 908 GGCATGTCGACGGCGGAGCTGCTGCTGAGCTTCAGCTGTCGCCCCNGTCGACACCTCTGAGGATTC 967
Db 964 GTATGGTACACAGAGKTCGCTGGTCAACTGGATGTCAGACATCTGGATCG 1023
QY 968 AGCGGTGAGGCTTCTTCAGCATGTCGCCCCNGTCGACACCTCTGAGGATTC 1027
Db 1024 AGCGGTGAGGACTGTCTTCAGCATGTCCTCTGAGGAGCTCTGAGGAGTGGC 1083
Db 1028 ATGAAAGAGGTGACCTGTCCTTCAGCATGTCCTCTGAGGAGCTGTGAG 1087
Db 1084 ATGAGAGGAGTACATGAGGAGCTGAGGAGCTGAGGAGCTGAGGAG 1143
QY 1088 GAGGACATCGCCAGGAGAAACCCCTCACCCAGGAGGAGCTGAGGAGCTGAG 1147
Db 1144 GAGACATCGCCAGGAGAAACCCCTCACCCGGAGGAGCTGAGGAGCTGAG 1203
QY 1148 GCTGTGACCTCTGAGCTGGCGCCAGGGAGTTGGCCCGACGGGGCTCCCTGTCGAGA 1207
Db 1204 GCCCAGCTCTGAGTGGCTCCAGGAGSTCTCAG - - - - - TCTGAGACTTGGAG 1259
QY 1208 CTTCGGACCCCTCGACCCAGAGGAGCTGAGGAGCTGAGGAGCTGAGGAG 1320
Db 1261 CTCCCGACCTCTGCTGAGCATCGAGTCCAGACATCTGTTCTGAGACTTGGAG 1319
QY 1260 AGAGATGGCCCAAGGAAATTAGAGAGSCTGAGGAGCTGAGGAGCTGAGGAG 1368
Db 1321 AGAGGGAGCTCTGGAGGACTCTGAGCTT - - - - - CGGAGACCTGGAGTG 1368
QY 1320 TGGCTGCTCTCTGAGGAGGCTCAGATTCACAAAGCTCTTAATCTCTCTAAATG 1379
Db 1369 TGGCTGCTCTCTGAGGAGGCTCAGATTCACAAAGCTCTTAATCTCTCTAAATG 1428
QY 1380 GGCTTCTCTGCTGCCCCCTCTGAGCTGGGGGGAGGTTGGACTTGGAAACAA 1439
Db 1429 GGCTTCTCTGCTGCTCTGAGCTGGGGAGTGGTGGAGCTAAGGAATGGA 1487
QY 1440 TATAAGA-----CATCTCATCATCACGGGGTGAAGGTGAGGAGCTT 1491
Db 1488 TCTCAAGGAGTATCTTTTTAACACAGGTTAAGGICAGATTAGGCAGCTT 1547
QY 1492 CTTCACAG 1499
Db 1548 CCTCAAG 1555

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RESULT 9
PCT-US02-31357-118
; Sequence 118, Application PCT-US0231357
; GENERAL INFORMATION:
; APPLICANT: Curagen Corporation, et al
; TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS OF USE
; FILE REFERENCE: 21402-462D-051
; CURRENT APPLICATION NUMBER: PCT-US02/31357
; PRIORITY APPLICATION NUMBER: 60/1327, 454
; PRIORITY FILING DATE: 2001-10-05
; PRIORITY APPLICATION NUMBER: 60/1328, 917
; PRIORITY FILING DATE: 2001-10-09
; PRIORITY APPLICATION NUMBER: 60/1328, 029
; PRIORITY FILING DATE: 2001-10-09
; PRIORITY APPLICATION NUMBER: 60/1328, 056
; PRIORITY FILING DATE: 2001-10-09
; PRIORITY APPLICATION NUMBER: 60/1328, 849
; PRIORITY FILING DATE: 2001-10-12
; PRIORITY APPLICATION NUMBER: 60/1329, 414
; PRIORITY FILING DATE: 2001-10-15
; PRIORITY APPLICATION NUMBER: 60/1330, 142
; PRIORITY FILING DATE: 2001-10-17
; PRIORITY APPLICATION NUMBER: 60/1341, 058
; PRIORITY FILING DATE: 2001-10-22
; PRIORITY APPLICATION NUMBER: 60/1343, 629
; PRIORITY FILING DATE: 2001-10-24
; PRIORITY APPLICATION NUMBER: 60/1349, 575
; PRIORITY FILING DATE: 2001-10-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 133
; SEQ ID NO: 118
; LENGTH: 2132
; SOFTWARE: CuraSeqList version 0.1

RESULT 10
US-10-262-445-118
; Sequence 118, Application US-10262445
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine
; APPLICANT: Alisbrook II, John
; APPLICANT: Catterton, Elina
; APPLICANT: Chant, John
; APPLICANT: Chaudhuri, Amitabha
; APPLICANT: Edinger, Shlomit
; APPLICANT: Gerlach, Valerie
; APPLICANT: Giot, Loic
; APPLICANT: Gorman, Linda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Mezes, Peter
; APPLICANT: Millet, Isabelle
; APPLICANT: Ooi, Chean Eng
; APPLICANT: Paturrajan, Meera
; APPLICANT: Ringer, Daniel
; APPLICANT: Spytek, Kimberly
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Zerhusen, Bryan

Query Match 29.6%; Score 515.6; DB 1; Length 2132;
Best Local Similarity 76.1%; Pred. No. 2; Be-121;
Matches 635; Conservative 0; Mismatches 199; Indels 0; Gaps 0;
QY 61 CATGGACCCATTCAAGCAGCAGAAGGTGGAGGACTTTATGACATCGGAGGAGGCTGG 120
Db 93 CATGCCAACGTTCAAGGAGGAGGACATTATGAGATGGGGAGGAGCTGG 152
QY 121 GAGTGGCCGATGTTGCCATCTGAGAAGTGGCCGGAGAGACACGGGCTGCTGAGATGC 180
Db 153 CAGCGGCCGATGTTGCCGAGGAGGAGGACGGGAGGAGGAGGCTGG 212
QY 721 CACGAAACGAGAACATCTGCAATACATGAGTAGGTTAGACTTGATGAGGATT 780
Db 753 GACCAAGCAGGAGAGACGCTTACACATCTACCGGTGAACTAGACTTGACAGGAGTA 812
QY 813 CTTCAGCAACACCGAGCTGGCCAGGACTCTATGCCGCTGTCAGATTCAGATCC 872
QY 841 CCGGAACAGCTCACAACTCAGAGGGCTTCAGACACCCCTGATCGGCCGTT 894
Db 873 CAAGGGAGAATGACCATGCCCCAGAGSCCTGGACATTCCTGGATTAAGGCGAT 926
QY 453 CAAGGAGATCTGGGGGTCATCTGCACTCTAGGCATCGCAACTTGACCT 512
Db 481 CAACCGAGAACATATGTTGAGCAGAATTCCATTCCACACATCAGCTGAT 540
Db 513 GAAGCGGAAACATCATGCTGCGACAGAACCTGCCAACCCAGCATCAAGCT 572
QY 541 TGACTTGGTGTGAGTCAGAAATAGAAGAGTGGAGCTGATTAAAGATTTGGAC 600
Db 573 CGACTTCGGCATGGCCACAGATCGAGGGGGAGCAGTCAGAACCTCTGGAC 632
QY 601 GCGCGGAATTGTTGCTCCAGAAATTGTTGACTACGAGCCCTGSGCTCTGAGCT 660
Db 633 CCCGGAGTTGTTGGCCCGAGAGTTGTAAGCTATAGCCGCTGGGCTCTGGAGGACAT 692
QY 661 GTGGGGCATAGGGCTCATCACTTACATCTTCTAAGTGGAGCATCCCTTCCTGGAGA 720
Db 693 GTGGGCACTGGTCATCACCTATTCCTCTGAGGCTGATCCGGCTCTGGGCA 752
QY 721 CACGAGCAGAACACTGCAATATCAGTCAGTGTGAGTTGAGGATT 780
Db 753 GACCAAGCAGGAGGCTCACCAAGAACATCTAGCGCTGAGACTACGCTTCAGAGGAGTA 812
QY 781 CTTCAGCAACACCGAGCTGGCCAGGACTCTATGCCGCTGTCAGATTCAGATCC 872
Db 813 CTTCAGCAACACCGAGCTGGCCAGGACTCTATGCCGCTGTCAGATTCAGATCC 894
QY 841 CCGGAACAGCTCACAACTCAGAGGGCTTCAGACACCCCTGATCGGCCGTT 894
Db 873 CAAGGGAGAATGACCATGCCCCAGAGSCCTGGACATTCCTGGATTAAGGCGAT 926
QY 181 NGCCNAGTCATCAAAGACGCGCAGAGCCCGCGCGCGCGCGCGCGCGCGCGCG 240

QY 661 GTGGAGGATAGGGCTCATACATCTTCTAAGTGGAGCATCCCTTCTGGAGA 720
Db 213 AGCCAGTTCATCAAGAAAGCGCCCGCTGTCATCCRQCCCGCGTGGTGGCGCGAGGA 272
QY 693 GTGGAGGATCGGTCTACCTATATCCTCTGAGCGCGTATCCCGGTCTGGCGCA 752
QY 241 GATCGAGCGGGAGGTTGAGCATCTCGGCGGGTGTGACCCACAAATGTCATCACCGTCGA 300
Db 273 GATCGAGCGGGAGTGAATCTCTGGGAGATCGGCCACACATCTCACCTGCA 332
QY 301 CGACTCTATGAGAACCCGAGGAGCTGACTCTCTGAGCTAGTGTCTGGAGGA 360
Db 333 CGACATCTCTGAGAACAGAGGAGCTGTCCTCATCTCTGGAGCTGTCCTGGCGGA 392
QY 361 GCTTCTGATTCCTGGCCAGAGAGAGGAGACTGAGTGGAGGAGGGCCACAGCTCAT 420
Db 393 GCTCTTGAATTCCTGGGAGAGAGAGGAGCTGAGGAGGAGGGCCACAGCTCAT 452
QY 421 TAACGAGATCTGGTGGGTTGAACTACATCTCACCAAGAAATGTCACTTGATCT 480
Db 453 CAAGGAGATCTGGGGGTCATCTGCACTCTAGGCATCGCAACTTGACCT 512
QY 481 CAACCGAGAACATATGTTGAGCAGAATTCCATTCCACACATCAGCTGAT 540
Db 513 GAAGCGGAAACATCATGCTGCGACAGAACCTGCCAACCCAGCATCAAGCT 572
QY 541 TGACTTGGTGTGAGTCAGAAATAGAAGAGTGGAGCTGATTAAAGATTTGGAC 600
Db 573 CGACTTCGGCATGGCCACAGATCGAGGGGGAGCAGTCAGAACCTCTGGAC 632
QY 601 GCGCGGAATTGTTGCTCCAGAAATTGTTGACTACGAGCCCTGSGCTCTGAGCT 660
Db 633 CCCGGAGTTGTTGGCCCGAGAGTTGTAAGCTATAGCCGCTGGGCTCTGGAGGACAT 692
QY 661 GTGGGGCATAGGGCTCATCACTTACATCTTCTAAGTGGAGCATCCCTTCCTGGAGA 720
Db 693 GTGGGCACTGGTCATCACCTATTCCTCTGAGGCTGATCCGGCTCTGGGCA 752
QY 721 CACGAGCAGAACACTGCAATATCAGTCAGTGTGAGTTGAGGATT 780
Db 753 GACCAAGCAGGAGGCTCACCAAGAACATCTAGCGCTGAGACTACGCTTCAGAGGAGTA 812
QY 781 CTTCAGCAACACCGAGCTGGCCAGGACTCTATGCCGCTGTCAGATTCAGATCC 872
Db 813 CTTCAGCAACACCGAGCTGGCCAGGACTCTATGCCGCTGTCAGATTCAGATCC 894
QY 841 CCGGAACAGCTCACAACTCAGAGGGCTTCAGACACCCCTGATCGGCCGTT 894
Db 873 CAAGGGAGAATGACCATGCCCCAGAGSCCTGGACATTCCTGGATTAAGGCGAT 926
QY 181 NGCCNAGTCATCAAAGACGCGCAGAGCCCGCGCGCGCGCGCGCGCGCGCG 240


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; RESULT 12
; US-09-724-676A-20895
; Sequence 20895, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 20895
; LENGTH: 2570
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: misc-feature
; NAME/KEY: misc-feature
; LOCATION: (5)..(5)
; OTHER INFORMATION: n is a,c,g, or t
; FEATURE: misc-feature
; NAME/KEY: misc-feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: n is a,c,g, or t
; US-09-724-676A-20895

Query Match 29.6%; Score 515.4; DB 6; Length 2570;
Best local similarity 76.4%; Pred. No. 3.4e-121; Mismatches 633; Conservative 0; Indels 0; Gaps 0; Matches 196; Mismatches 0; Insertions 0; Gaps 0;

; RESULT 13
; US-09-724-676-20893
; Sequence 20893, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 20893
; LENGTH: 979
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: misc-feature
; NAME/KEY: misc-feature
; LOCATION: (5)..(5)
; OTHER INFORMATION: n is a,c,g, or t
; FEATURE: misc-feature
; NAME/KEY: misc-feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: n is a,c,g, or t
; US-09-724-676A-20895

Query Match 29.6%; Score 515.4; DB 6; Length 2570;
Best local similarity 76.4%; Pred. No. 3.4e-121; Mismatches 633; Conservative 0; Indels 0; Gaps 0; Matches 196; Mismatches 0; Insertions 0; Gaps 0; Matches 191; Mismatches 132; Insertions 61; Gaps 0;

; RESULT 14
; US-09-724-676-20894
; Sequence 20894, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 20894
; LENGTH: 979
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: misc-feature
; NAME/KEY: misc-feature
; LOCATION: (5)..(5)
; OTHER INFORMATION: n is a,c,g, or t
; FEATURE: misc-feature
; NAME/KEY: misc-feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: n is a,c,g, or t
; US-09-724-676A-20895

Query Match 29.6%; Score 515.4; DB 6; Length 2570;
Best local similarity 76.4%; Pred. No. 3.4e-121; Mismatches 633; Conservative 0; Indels 0; Gaps 0; Matches 196; Mismatches 0; Insertions 0; Gaps 0; Matches 191; Mismatches 132; Insertions 61; Gaps 0;

; RESULT 15
; US-09-724-676-20895
; Sequence 20895, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 20895
; LENGTH: 979
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: misc-feature
; NAME/KEY: misc-feature
; LOCATION: (5)..(5)
; OTHER INFORMATION: n is a,c,g, or t
; FEATURE: misc-feature
; NAME/KEY: misc-feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: n is a,c,g, or t
; US-09-724-676A-20895

Query Match 29.6%; Score 515.4; DB 6; Length 2570;
Best local similarity 76.4%; Pred. No. 3.4e-121; Mismatches 633; Conservative 0; Indels 0; Gaps 0; Matches 196; Mismatches 0; Insertions 0; Gaps 0; Matches 191; Mismatches 132; Insertions 61; Gaps 0;

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 Db 672 CCCGAGATTTGGCTCCAGAGATTTGTGAACTACAGGCCCTGGCTGGAGGGTGAC 731
 QY 661 GTGGAGCATAGGCCATCACCTCATCCCTTAACTTGTGAGGATCCCCTTCCCTGGAGA 720
 Db 732 GTGGAGCATGGCTCATCACCTATCTCTGGCTGATCCCCTTCCCTGGAGA 791
 QY 721 CACCAAGAGGAACACTGCAAAATCACATCATGAGTTACACTTGTGAGGAATT 780
 Db 792 GACCAAGAGGAACCTGCAAAATCACATCATGAGTTACACTTGTGAGGAATT 851
 QY 781 CTCAGGCCATACAGCCGGAGCTGGCAAGGACTTTATCGGAAGTTCTGGTAAAGAGAC 840
 Db 852 CTCAGCACACCCGGAGGCTGGCAAGGACTTCATCCGGTGTGTCAGAGATCC 911
 QY 841 CGGAAACGGCTCACAATCCAAAGGGCTGCTCAGCACCCCTGGAT 885
 Db 912 CAAGCGGAGAATGACATGCCAGGCCCTGGAAQATTCTGGAT 956

RESULT 15

US-10-144-771-9285

Sequence 9285, Application US/10144771

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig

TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF

FILE REFERENCE: CL001321

CURRENT APPLICATION NUMBER: US/10/144,771

NUMBER OF SEQ ID NOS: 47235

SEQ ID NO: 9385

LENGTH: 1410

TYPE: DNA

ORGANISM: HUMAN

US-10-144-771-9285

Query Match 29.5%; Score 513.8; DB 8; Length 1410;
 Best Local Similarity 76.2%; Pred. No. 6.9e-121; Mismatches 0; Indels 0; Gaps 0;

Matches 632; Conservative 0; Mismatches 197; Indels 0; Gaps 0;

QY 61 CATTGAGGCCATTCAAGCAGCAAGGAGGTGGAGACTTGTGAGGAGGCTGG 120
 Db 9 CATTGAGGCCATTCAAGCAGCAAGGAGGTGGAGACTTGTGAGGAGGCTGG 68

QY 121 GAGGGCCAGTTGCATCTGGAAAGAGTCCGGAGAAGAGCAGCGGGCTTGATGATGC 180
 Db 69 CAGTGGCCATTTCATCTGGCCAAAGTGGCAAGAGGGCAGGGATGGTATGC 128

QY 181 AGCCAGTTCATCAAGAAGCGGCGAGCCGGCGAGGCGCTGGTGAAGCCGAGA 240
 Db 129 AGCCAGTTCATCAAGAAGCGGCGCTGGCATCCAGCCGGCGGTGAGCCGGAGGA 188

QY 241 GATGGAGCGGGAGGTGAGACATCTGGGGAGGCTGCAACATGTCATCGCTCA 300
 Db 189 GATGGAGCGGGAGGTGAGCATCTGGGGAGGCTGCAACATGTCATCGCTCA 248

QY 301 CGAGCTCTATGAGAACGCCAACGGAGCTGGTGCACATCTGGAGTAGTGTGGAGGA 360
 Db 249 TGAAGTGTGAGAACAGAACAGATGTGGGGCTGCAACATGTCATCGCTCA 308

QY 361 GCTCTGAGATTCTGGATGGGGTGAACCTTCAGAACAGAAATTGTGCACTTGTACCT 480
 Db 369 CAAGAACATCTGAGGGCTCCACTACCTGACTCCAGGCATCGCACACTTGACCT 428

QY 481 CAAGCCAGAACATTATGTTGAGAACATAATCCGATTGACAGACAGACAGTGAT 540
 Db 429 GAAGCCGAGAACATCATGTTGCTGGACAAAGCACAGCAGCAGGCCGCCCCGATTAGCTCAT 488

QY 541 TGAATTGGCTGTGACTCACGAAATAAGAAGATGGAGGTGAATTAGAATTTGGAC 600
 Db 489 CGACITTGCCATCGCCAGAGATCGGGCTGGCTGGAGGCTGAGACATCTTGAC 548

QY 601 GCGCGAATTGTGCTCCAGAAATTGTGAACTACAGGCCCTGGCTGGAGGGTGAC 660
 Db 549 ACCGGAGTTGTGCTCCAGAAATTGTGACTACAGGCCCTGGCTGGAGGCTGAC 608

QY 661 GTGGAGCATGGCTCATCACCTATCTCTGGCTGATCCCCTTCCCTGGAGA 720
 Db 721 CACCAAGAGGAACACTGCAAAATCACATCATGAGTTACACTTGTGAGGAATT 780

QY 781 CTCAGGCCATACAGCCGGAGCTGGCAAGGACTTCATCCGGTGTGTCAGAGATCC 791
 Db 609 GTGGAGCATGGCTCATCACCTACATCTCTGGAGATCGTGAACATGTGAGGACTTCAGGGTGAAT 668

QY 721 CACGAAGAGGAAACCTGGAAATATCACATCAGTGTGAGTTACACTTGTGAGGAATT 780
 Db 669 GACCAAGAGGAGGCTGAGACATCTGGAGTGAACATCTGGAGTGAACTTGTGAGGATA 728

QY 781 CTCAGGCCATACAGCCGGAGCTGGCAAGGACTTCATCCGGTGTGTCAGAGATCC 788
 Db 729 CTCAGCAGGACCAAGCAGGGCTGSCCAAGGACTTTATGGGAAGCTTCTGGTTAAAGAGAC 840

QY 841 CGGAAACGGCTCACAATCCAAAGGGCTCAGCACCCCTGGATCAG 889
 Db 789 CAAGAGGAGATGACATGCCACAGGAGCTGGAGCATCTGGATCAAG 837

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GenCore version 5.1.3
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OM nucleic - nucleic search, using SW model

Run on:

April 4, 2003, 19:24:37 ; Search time 370.763 Seconds

(without alignments) 8137.548 Million cell. updates/sec

Title: US-09-719-748-1_COPY_1022_1141

Perfect score: 120

Sequence: 1 tcgcgttggaaagggtgca.....ggagggggcagcaccc 120

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the best being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	120	100.0	454	16	US-09-234-611-14012		Sequence 14012, A
2	120	100.0	454	16	US-09-234-076-19174		Sequence 19174, A
3	120	100.0	454	16	US-09-289-768-21173		Sequence 21173, A
4	120	100.0	454	17	US-09-332-782-19174		Sequence 19174, A
5	120	100.0	454	29	US-09-737-223-19174		Sequence 19174, A
6	120	100.0	454	34	US-09-904-809-14012		Sequence 14012, A
7	120	100.0	454	34	US-09-918-995-19174		Sequence 19174, A
8	120	100.0	454	34	US-09-933-397-21173		Sequence 21173, A
9	120	100.0	480	29	US-09-757-982-12		Sequence 12, Appl
10	120	100.0	1253	1	PCT-US01-08631-9265		Sequence 9265, Appl
11	120	100.0	1451	16	PCT-US09-27149-176		Sequence 176, Appl
12	120	100.0	1451	33	US-09-891-825-176		Sequence 176, Appl
13	120	100.0	1512	25	US-09-649-163-7647		Sequence 7647, Appl
14	120	100.0	1512	25	US-09-655-816-8022		Sequence 8022, Appl
15	120	100.0	1512	25	US-09-652-913-8169		Sequence 8169, Appl
16	120	100.0	1512	25	US-09-652-917-2793		Sequence 2793, Appl
17	120	100.0	1742	1	PCT-US09-1341-1		Sequence 1, Appl
18	120	100.0	1742	1	PCT-US09-1341-1		Sequence 1, Appl
19	120	100.0	1742	28	US-09-719-948-1		Sequence 1, Appl
20	120	100.0	1864	29	US-09-757-982-19		Sequence 19, Appl
21	100.0	2235	23	US-09-606-776-3799		Sequence 3799, Appl	

22 120 100.0 2235 25 US-09-649-163-9895
 Sequence 9895, AP ; CURRENT FILING DATE: 1999-01-20
 23 120 100.0 2235 25 US-09-652-917-3775 ; NUMBER OF SEQ ID NOS: 38054
 Sequence 12255, A ; SOFTWARE: FASTSEQ for Windows Version 3.0
 24 120 100.0 2235 27 US-09-698-010-12235 ; SEQ ID NO 19174
 Sequence 6041, AP ; LENGTH: 454
 25 120 100.0 2235 27 US-09-698-011-6041 ; TYPE: DNA
 Sequence 2005, AP ; ORGANISM: Homo sapiens
 26 119 99.2 242 11 US-08-705-765-907 ; FEATURE: misc_feature
 Sequence 20051, AP ; NAME/KEY: misc_feature
 27 109 90.8 362 13 US-08-975-985-2005 ; LOCATION: (1)..(454)
 Sequence 30021, AP ; OTHER INFORMATION: n = A,T,C or G
 28 109 90.8 362 34 US-09-912-292-30021 ; US-09-235-076-19174
 Sequence 3329, AP ;
 29 105 88.3 1970 71 US-60-278-232-3329 ;
 Sequence 33291, AP ;
 30 99.2 82.7 279 20 US-09-539-806-4775 ;
 Sequence 47575, A ;
 31 97.5 81.3 1732 80 US-60-360-207-3361 ;
 Sequence 3361, AP ;
 32 85.6 71.3 422 27 US-09-698-010-6454 ;
 Sequence 6454, AP ;
 33 80.4 67.0 495 25 US-09-652-816-4516 ;
 Sequence 4515, AP ;
 34 80.4 67.0 496 21 US-09-540-229-137005 ;
 Sequence 137005, AP ;
 35 79.4 66.2 434 19 US-09-528-409-88315 ;
 Sequence 88315, A ;
 36 79.4 66.2 434 35 US-09-933-524-88315 ;
 Sequence 88315, A ;
 37 79.4 66.2 434 35 US-09-933-524-88315 ;
 Sequence 883151, A ;
 38 78.8 65.7 635 62 US-60-182-093-1080 ;
 Sequence 1080, AP ;
 39 78.8 65.0 377 21 US-09-540-766-33879 ;
 Sequence 5879, A ;
 40 77.4 64.5 284 11 US-82-035-1455 ;
 Sequence 1455, AP ;
 41 77.4 64.5 284 21 US-09-540-212A-37909 ;
 Sequence 37909, A ;
 42 59 49.2 219 12 US-08-869-540-261 ;
 Sequence 261, APP ;
 43 59 49.2 219 45 US-60-181-911-261 ;
 Sequence 261, APP ;
 44 59 49.2 345 23 US-09-616-082-268 ;
 Sequence 268, APP ;
 45 58.4 48.7 332 18 US-09-411-587-970 ;
 Sequence 970, APP ;
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ALIGNMENTS

RESULT 1
 US-09-234-611-14012 ; Sequence 14012, Application US/09234611
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq, Inc.
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
 ; FROM VARIOUS CDNA LIBRARIES
 ; FILE REFERENCE: 20411-757
 ; CURRENT APPLICATION NUMBER: US/09/234,611
 ; CURRENT FILING DATE: 1999-01-21
 ; NUMBER OF SEQ ID NOS: 21025
 ; SOFTWARE: FASTSEQ for Windows Version 3.0
 ; SEQ ID NO 14012
 ; LENGTH: 454
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(454)
 ; OTHER INFORMATION: n = A,T,C or G
 ; US-09-234-611-14012

Query Match 100.0%; Score 120; DB 16; Length 454;
 Best Local Similarity 100.0%; Pred. No. 1. 7e-22;
 Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGCTGATGAGAAGGGTGCACCTGAGGACTGTGAGATGAC 60
 Db 266 TCGCTGATGAGAAGGGTGCACCTGAGGACTGTGAGATGAC 325

Qy 61 ACTGAGGAGGACATGCCAGGAGAACCCCTACCCACGGAGGAGGACCTCC 120
 Db 326 ACTGAGGAGGACATGCCAGGAGAACCCCTACCCACGGAGGAGGACCTCC 385

RESULT 3
 US-09-289-768-21173 ; Sequence 21173, Application US/09289768
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq, Inc.
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
 ; FROM VARIOUS CDNA LIBRARIES
 ; FILE REFERENCE: 20411-765
 ; CURRENT APPLICATION NUMBER: US/09/289, 768
 ; CURRENT FILING DATE: 1999-04-08
 ; NUMBER OF SEQ ID NOS: 31996
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 21173
 ; LENGTH: 454
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(454)
 ; OTHER INFORMATION: n = A,T,C or G
 ; US-09-289-768-21173

Query Match 100.0%; Score 120; DB 16; Length 454;
 Best Local Similarity 100.0%; Pred. No. 1. 7e-22;
 Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGCTGATGAGAAGGGTGCACCTGAGGAGGACTGTGAGATGAC 60
 Db 266 TCGCTGATGAGAAGGGTGCACCTGAGGAGGACTGTGAGATGAC 325

RESULT 4
 US-09-332-782-19174 ; Sequence 19174, Application US/09332782A
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq, Inc.
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
 ; FROM VARIOUS CDNA LIBRARIES
 ; FILE REFERENCE: 20411-756
 ; CURRENT APPLICATION NUMBER: US/09/332,782A
 ; CURRENT FILING DATE: 1999-06-14
 ; NUMBER OF SEQ ID NOS: 38054
 ; SOFTWARE: FASTSEQ for Windows Version 3.0

RESULT 2
 US-09-235-076-19174 ; Sequence 19174, Application US/09235076
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq, Inc.
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
 ; FROM VARIOUS CDNA LIBRARIES
 ; FILE REFERENCE: 20411-756
 ; CURRENT APPLICATION NUMBER: US/09/235,076

Query Match 100.0%; Score 120; DB 16; Length 454;
 Best Local Similarity 100.0%; Pred. No. 1. 7e-22;
 Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGCTGATGAGAAGGGTGCACCTGAGGACTGTGAGATGAC 60
 Db 266 TCGCTGATGAGAAGGGTGCACCTGAGGACTGTGAGATGAC 325

Qy 61 ACTGAGGAGGACATGCCAGGAGAACCCCTACCCACGGAGGAGGACCTCC 120
 Db 326 ACTGAGGAGGACATGCCAGGAGAACCCCTACCCACGGAGGAGGACCTCC 385

SEQ ID NO 19174

LENGTH: 454

ORGANISM: Homo sapiens

FEATURE: misc_feature

LOCATION: (1)..(454)

OTHER INFORMATION: n = A,T,C or G

US-09-332-782-19174

Query Match 100.0%; Score 120; DB 17; Length 454;

Best Local Similarity 100.0%; Pred. No. 1.7e-22; Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGCTGATGAGAGGGTGCACCTGAGGAGCTGAGGAACCTGAGAGTCAC 60
 Db 266 TCGCTGATGAGAGGGTGCACCTGAGGAGCTGAGGAACCTGAGAGTCAC 325

Qy 61 ACTGAGGAGGACATGCCAGGAGGAAACCCCTCACCACCGAGGAGGAGCCTCC 120
 Db 326 ACTGAGGAGGACATGCCAGGAGGAAACCCCTCACCACCGAGGAGGAGCCTCC 385

RESULT 5

US-09-737-223-19174

Sequence 19174, Application US/09737223

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

FROM VARIOUS CDNA LIBRARIES

FILE REFERENCE: 20411-756

CURRENT APPLICATION NUMBER: US/09/737,223

CURRENT FILING DATE: 2000-12-13

PRIOR APPLICATION NUMBER: 09/332,782

PRIOR FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 38054

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 19174

LENGTH: 454

FEATURE: misc_feature

LOCATION: (1)..(454)

OTHER INFORMATION: n = A,T,C or G

US-09-737-223-19174

Query Match 100.0%; Score 120; DB 29; Length 454;

Best Local Similarity 100.0%; Pred. No. 1.7e-22; Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGCTGATGAGAGGGTGCACCTGAGGAGCTGAGGAACCTGAGAGTCAC 60
 Db 266 TCGCTGATGAGAGGGTGCACCTGAGGAGCTGAGGAACCTGAGAGTCAC 325

Qy 61 ACTGAGGAGGACATGCCAGGAGGAAACCCCTCACCACCGAGGAGGAGCCTCC 120
 Db 326 ACTGAGGAGGACATGCCAGGAGGAAACCCCTCACCACCGAGGAGGAGCCTCC 385

RESULT 6

US 09-904-809-14012

Sequence 14012, Application US/09904809

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: NOVEL NUCLEAR ACID SEQUENCES OBTAINED

FROM VARIOUS CDNA LIBRARIES

FILE REFERENCE: 20411-757

CURRENT APPLICATION NUMBER: US/09/904,809

PRIOR APPLICATION NUMBER: 09/234,611

PRIOR FILING DATE: 1999-01-22

NUMBER OF SEQ ID NOS: 21025

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 14012

LENGTH: 454

ORGANISM: Homo sapiens

FEATURE: misc_feature

LOCATION: (1)..(454)

OTHER INFORMATION: n = A,T,C or G

US-09-904-809-14012

Query Match 100.0%; Score 120; DB 34; Length 454;

Best Local Similarity 100.0%; Pred. No. 1.7e-22; Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGCTGATGAGAGGGTGCACCTGAGGAGCTGAGGAACCTGAGAGTCAC 60
 Db 266 TCGCTGATGAGAGGGTGCACCTGAGGAGCTGAGGAACCTGAGAGTCAC 325

Qy 61 ACTGAGGAGGACATGCCAGGAGGAAACCCCTCACCACCGAGGAGGAGCCTCC 120
 Db 326 ACTGAGGAGGACATGCCAGGAGGAAACCCCTCACCACCGAGGAGGAGCCTCC 385

RESULT 7

US-09-918-995-19174

Sequence 19174, Application US/09918995

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

FROM VARIOUS CDNA LIBRARIES

FILE REFERENCE: 20411-756

CURRENT APPLICATION NUMBER: US/09/918,995

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US/09/235,076

PRIOR FILING DATE: 1999-01-20

NUMBER OF SEQ ID NOS: 38054

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 19174

LENGTH: 454

FEATURE: misc_feature

LOCATION: (1)..(454)

OTHER INFORMATION: n = A,T,C or G

US-09-918-995-19174

Query Match 100.0%; Score 120; DB 34; Length 454;

Best Local Similarity 100.0%; Pred. No. 1.7e-22; Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGCTGATGAGAGGGTGCACCTGAGGAGCTGAGGAACCTGAGAGTCAC 60
 Db 266 TCGCTGATGAGAGGGTGCACCTGAGGAGCTGAGGAACCTGAGAGTCAC 325

Qy 61 ACTGAGGAGGACATGCCAGGAGGAAACCCCTCACCACCGAGGAGGAGCCTCC 120
 Db 326 ACTGAGGAGGACATGCCAGGAGGAAACCCCTCACCACCGAGGAGGAGCCTCC 385

RESULT 8

US 09-939-397-21173

Sequence 21173, Application US/0939397

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

FROM VARIOUS CDNA LIBRARIES

FILE REFERENCE: 20411-765

CURRENT APPLICATION NUMBER: US/09/939,397

CURRENT FILING DATE: 2001-08-24

PRIOR APPLICATION NUMBER: 09/289,768

PRIOR FILING DATE: 1999-04-08

SEQ ID NO 176
LENGTH: 1451
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: All occurrences of n = any nucleotide

US-09-891-825-176

Query Match 100.0%; Score 120; DB 33; Length 1451;
Best Local Similarity 100.0%; Pred. No. 2e-22; 0; Mismatches 120; Conservative 0; Indels 0; Gaps 0;

Qy 1 TCGTGTGATGAGAAGGTGACCTGAGGACTGTGAGAGTGAC 60
Db 636 TCGTGTGATGAGAAGGTGACCTGAGGACTGTGAGAGTGAC 695

Qy 61 ACTCAGGAGGACATGCCAGGAGGAAGCCTCCACCCACGGAGGAGCACCTCC 120
Db 702 ACTGAGGAGGACATGCCAGGAGGAAGCCTCCACCCACGGAGGAGGAGCACCTCC 761

RESULT 13
US-09-649-163-7647
; Sequence 7617, Application US/09649163
GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas A.
APPLICANT: Galvin, Katherine A.
APPLICANT: Leiby, Kevin R.
APPLICANT: Kingbury, Gillian A.
APPLICANT: Welch, Nadine S.
APPLICANT: McCarthy, Sean A.
APPLICANT: Williamson, Mark
APPLICANT: Richardson, Jennifer
APPLICANT: MacBeth, Kyle J.
APPLICANT: Frazer, Christopher C.
APPLICANT: Villeval, Jean-Luc M.G.
APPLICANT: Goodearl, Andrew D.J.
APPLICANT: Silos-Santiago, Inmaculada
APPLICANT: White, David
APPLICANT: Pan, Yang
APPLICANT: Busfield, Samantha J.
APPLICANT: Dees, James
APPLICANT: Lee, John
APPLICANT: Shyian, Andrew W.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
FILE REFERENCE: 1600-1164-001
CURRENT APPLICATION NUMBER: US/09/649,163
CURRENT FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: 60/150,608
PRIOR FILING DATE: 1999-08-25
NUMBER OF SEQ ID NOS: 10535
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7647
LENGTH: 1512
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(1512)
; OTHER INFORMATION: n = A,T,C or G

US-09-649-163-7647

Query Match 100.0%; Score 120; DB 25; Length 1512;
Best Local Similarity 100.0%; Pred. No. 2e-22; 0; Mismatches 120; Conservative 0; Indels 0; Gaps 0;

Qy 1 TCGTGTGATGAGAAGGTGACCTGAGGACTGTGAGAGTGAC 60
Db 636 TCGTGTGATGAGAAGGTGACCTGAGGACTGTGAGAGTGAC 695

Qy 61 ACTCAGGAGGACATGCCAGGAGGAAGCCTCCACCCACGGAGGAGGAGCACCTCC 120
Db 702 ACTGAGGAGGACATGCCAGGAGGAAGCCTCCACCCACGGAGGAGGAGGAGCACCTCC 761

RESULT 14
US-09-652-816-8022
; Sequence 8022, Application US/09652816
GENERAL INFORMATION:
APPLICANT: Gutierrez-Ramos, Jose-Carlos
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
FILE REFERENCE: 1600-1177-001
CURRENT FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,111
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 9647
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8022
LENGTH: 1512
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(1512)
; OTHER INFORMATION: n = A,T,C or G

US-09-652-816-8022

Query Match 100.0%; Score 120; DB 25; Length 1512;
Best Local Similarity 100.0%; Pred. No. 2e-22; 0; Mismatches 120; Conservative 0; Indels 0; Gaps 0;

Qy 1 TCGTGTGATGAGAAGGTGACCTGAGGACTGTGAGAGTGAC 60
Db 636 TCGTGTGATGAGAAGGTGACCTGAGGACTGTGAGAGTGAC 695

Qy 61 ACTCAGGAGGACATGCCAGGAGGAAGCCTCCACCCACGGAGGAGGAGCACCTCC 120
Db 702 ACTGAGGAGGACATGCCAGGAGGAAGCCTCCACCCACGGAGGAGGAGGAGCACCTCC 761

RESULT 15
US-09-652-913-8169
; Sequence 8169, Application US/09652913
GENERAL INFORMATION:
APPLICANT: Faib, Dean R.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
FILE REFERENCE: 1600-1174-001
CURRENT APPLICATION NUMBER: US/09/652,913
CURRENT FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,107
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 10833
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8169
LENGTH: 1512
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(1512)
; OTHER INFORMATION: n = A,T,C or G

US-09-652-913-8169

Query Match 100.0%; Score 120; DB 25; Length 1512;
Best Local Similarity 100.0%; Pred. No. 2e-22; 0; Mismatches 120; Conservative 0; Indels 0; Gaps 0;

Qy 1 TCGTGTGATGAGAAGGTGACCTGAGGACTGTGAGAGTGAC 60
Db 636 TCGTGTGATGAGAAGGTGACCTGAGGACTGTGAGAGTGAC 695

Qy 61 ACTCAGGAGGACATGCCAGGAGGAAGCCTCCACCCACGGAGGAGGAGCACCTCC 120
Db 702 ACTGAGGAGGACATGCCAGGAGGAAGCCTCCACCCACGGAGGAGGAGGAGCACCTCC 761

Wed Apr 9 09:37:53 2003

us-09-719-748-1_copy_1022_1141.rnlpm

Page 6

Db 696 |||||||ACTGAGGAGGACATGCCAGGAGAAAGCCCTCCACCCACGGAGAGGAGACCTCC 755

Search completed: April 4, 2003, 22:30:07
Job time : 372.763 secs

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Om nucleic - nucleic search, using sw model

Run on:

April 4, 2003, 20:49:32 ; Search time 64.8335 Seconds

7198.356 Million cell updates/sec

Title: US-09-719-748-1_COPY_1022_1141

Perfect score: 120

Sequence: 1 tcgcgtatggaaagggtc.....ggagggaggcagcaccc 120

Scoring table: IDENTITY_NUC

GapOp 10.0 , Gapext 1.0

Searched: 5575038 seqs, 1944561127 residues

Total number of hits satisfying chosen parameters: 11150076

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Pending Patents NA New:*

1: /cggn2_6/podata/2/pna/pct NEW COMB. seq: *
2: /cggn2_6/podata/2/pna/US06 NEW COMB. seq: *
3: /cggn2_6/podata/2/pna/US07 NEW COMB. seq: *
4: /cggn2_6/podata/2/pna/US08 NEW COMB. seq: *
5: /cggn2_6/podata/2/pna/US09 NEW COMB. seq: *
6: /cggn2_6/podata/2/pna/US09 NEW COMB. seq2: *
7: /cggn2_6/podata/2/pna/US10 NEW COMB. seq: *
8: /cggn2_6/podata/2/pna/US10 NEW COMB. seq2: *
9: /cggn2_6/podata/2/pna/US60 NEW COMB. seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	120	100.0	1442	6	US-09-724-676-34736
C 2	120	100.0	1442	6	US-09-724-676A-34736
C 3	120	100.0	2085	9	US-50-43-566-647
C 4	99.2	82.7	279	5	US-09-539-806B-47575
C 5	97.6	81.3	1732	8	US-11-144-772-3361
C 6	96.8	80.7	649	8	US-10-33-044-386
C 7	80.4	67.0	601	5	US-09-947-907-15359
C 8	80.4	67.0	1195	1	PCT-US03-01096-36
C 9	61	50.8	201	9	US-60-43-566-10041
C 10	51.6	43.0	609	8	US-10-266-131-2686
C 11	33.4	27.8	3373	7	US-10-388-360-2334
C 12	32.2	26.8	595	8	US-10-264-237-1083
C 13	32.2	26.8	891	9	US-60-452-680-6448
C 14	32.2	26.8	1160	9	US-60-452-680-6447
C 15	32.2	26.8	1923	6	US-09-620-312D-1004
C 16	32.2	26.8	1923	7	US-10-117-722-1004
C 17	32.2	26.8	1994	9	US-60-452-680-6451
C 18	32.2	26.8	2655	9	US-60-452-680-6450
C 19	32.2	26.8	888463	5	US-09-947-911-117
C 20	32.2	26.8	3037227	5	US-09-947-911-286
C 21	31.8	26.5	3415	9	US-60-443-566-1019
C 22	31.8	26.5	3415	9	US-60-453-135-7496
C 23	31.8	26.3	387	7	US-10-304-123A-8205
C 24	31.4	26.2	311	8	US-10-144-771-5116

RESULT 1
US-09-724-676-34736/C
; Sequence 34736, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34736
; LENGTH: 1442
; TYPE: DNA
; ORGANISM: Homo sapiens
; - ORGANISM: Homo sapiens
US-09-724-676A-20442
; ALIGNMENTS

Query Match 100.0%; Score 120; DB 6; Length 1442;
Best Local Similarity 100.0%; Pred. No. 1.8e-24;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGGTGATGAGAGGAGTCACCTGAGGAGCTGAGAGTCAC 60
Db 414 TCGGTGATGAGAGGAGTCACCTGAGGAGCTGAGAGTCAC 355

QY 61 ACTGGAGGAGCATGCCAGGAGAACCCCTACCCACGGAGGAGCCTCC 120
Db 354 ACTGGAGGAGCATGCCAGGAGAACCCCTACCCACGGAGGAGCCTCC 295

RESULT 2
US-09-724-676A-34736/C
; Sequence 34736, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34736
; LENGTH: 1442
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-34736

Query Match 100.0%; Score 120; DB 6; Length 1442;
 Best Local Similarity 100.0%; Pred. No. 1.8e-24;
 Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGCTGATGAGAAGGTGACCTCTAGGCCGATAGGACTGTGAGGTGAC 60
 Db 414 TCGCTGATGAGAAGGTGACCTCTAGGCCGATAGGACTGTGAGGTGAC 355
 Qy 61 ACTGGAGGACATGCCAGGAGAAAGCCTCACCCACGGAGGAGGACCTCC 120
 Db 354 ACTGGAGGACATGCCAGGAGAAAGCCTCACCCACGGAGGAGGACCTCC 295

RESULT 3
 US-09-443-566-647
 ; Sequence 647 Application US/60443566
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele
 ; APPLICANT: BEGOVICH, Ann
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; FILE REFERENCE: CL001447
 ; CURRENT APPLICATION NUMBER: US/60/443,566
 ; NUMBER OF SEQ ID NOS: 25102
 ; SEQ ID NO: 647
 ; LENGTH: 2085
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-60-443-566-647

Query Match 100.0%; Score 120; DB 9; Length 2085;
 Best Local Similarity 100.0%; Pred. No. 1.9e-24; Mismatches 0; Indels 0; Gaps 0;
 Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGCTGATGAGAAGGTGACCTCTAGGCCGATAGGACTGTGAGGTGAC 60
 Db 1029 TCGCTGATGAGAAGGTGACCTCTAGGCCGATAGGACTGTGAGGTGAC 1088

Qy 61 ACTGGAGGACATGCCAGGAGAAAGCCTCACCCACGGAGGAGGACCTCC 120
 Db 1089 ACTGGAGGACATGCCAGGAGAAAGCCTCACCCACGGAGGAGGACCTCC 1148

RESULT 4
 US-09-539-806B-4755
 ; Sequence 4755 Application US/09539806B
 ; GENERAL INFORMATION:
 ; APPLICANT: Seilhamer, Jeffrey J.
 ; APPLICANT: Deleageane, Angelo M.
 ; APPLICANT: Stuart, Susan G.
 ; APPLICANT: Stuve, Laura L.
 ; APPLICANT: Mullahy, Sara J.
 ; APPLICANT: Naughton, Rebecca E.
 ; TITLE OF INVENTION: POLYNUCLEOTIDES OF EXOCRINE GLAND TISSUE
 ; FILE REFERENCE: PD-1027 CIP
 ; CURRENT APPLICATION NUMBER: US/09/539,806B
 ; CURRENT FILING DATE: 2000-03-30
 ; PRIOR APPLICATION NUMBER: 08/705,766
 ; PRIOR FILING DATE: September 27, 1996
 ; PRIOR APPLICATION NUMBER: 60/104,676
 ; PRIOR FILING DATE: October 2, 1995
 ; PRIOR APPLICATION NUMBER: 08/749,515
 ; PRIOR FILING DATE: November 15, 1996
 ; PRIOR APPLICATION NUMBER: 60/006,810
 ; PRIOR FILING DATE: November 15, 1995
 ; PRIOR APPLICATION NUMBER: 08/722,285
 ; PRIOR FILING DATE: March 20, 1997
 ; PRIOR APPLICATION NUMBER: 60/103,696
 ; PRIOR FILING DATE: March 20, 1996
 ; PRIOR APPLICATION NUMBER: 08/931,197
 ; PRIOR FILING DATE: October 1, 1997

RESULT 5
 US-10-144-771-3361
 ; Sequence 3361 Application US/10144771
 ; GENERAL INFORMATION:
 ; APPLICANT: VENNER, J. Craig
 ; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
 ; FILE REFERENCE: CL001321
 ; CURRENT APPLICATION NUMBER: US/10/144,771
 ; CURRENT FILING DATE: 2002-05-15
 ; NUMBER OF SEQ ID NOS: 47235
 ; SEQ ID NO: 3361
 ; LENGTH: 1732
 ; TYPE: DNA
 ; ORGANISM: HUMAN
 ; US-10-144-771-3361

Query Match 82.7%; Score 99.2; DB 5; Length 279;
 Best Local Similarity 89.2%; Pred. No. 9.9e-19; Mismatches 13; Indels 0; Gaps 0;
 Matches 107; Conservative 89.2%; Mismatches 13; Indels 0; Gaps 0;

Qy 1 TCGCTGATGAGAAGGTGACCTCTAGGCCGCGATAGGACTGTGAGGTGAC 60
 Db 76 TCCCTGATGAGAAGGGGCACTGTGAGGACAAGTGAGGACCTGTGAGGTGAC 135

Qy 61 ACTGGAGGACATGCCAGGAGAAAGCCTCACCCACGGAGGAGGACCTCC 120
 Db 136 ACTGGAGGACATGCCAGGAGAAAGCCTCACCCACGGAGGAGGACCTCC 195

RESULT 6
 US-10-338-044-386/C
 ; Sequence 386 Application US/10338044
 ; GENERAL INFORMATION:
 ; APPLICANT: MENDICK, Donna
 ; APPLICANT: PORTER, Mark
 ; APPLICANT: JOHNSON, Kory
 ; APPLICANT: HIGGS, Brandon
 ; APPLICANT: CASTLE, Arthur

APPLICANT: BLASCHOFF, Michael
FILE REFERENCE: 4921-500-01-US
CURRENT APPLICATION NUMBER: US/10/1338,044
PRIORITY APPLICATION NUMBER: US 60/303,819
PRIORITY FILING DATE: 2001-07-10
PRIORITY APPLICATION NUMBER: US 60/305,623
PRIORITY FILING DATE: 2001-07-17
PRIORITY APPLICATION NUMBER: US 60/369,351
PRIORITY FILING DATE: 2002-04-03
PRIORITY APPLICATION NUMBER: US 60/377,611
PRIORITY FILING DATE: 2002-05-06
NUMBER OF SEQ ID NOS: 2696
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 386
LENGTH: 649
TYPE: DNA
ORGANISM: *Rattus norvegicus*
FEATURE: OTHER INFORMATION: Genbank Accession No. AAB92388
US-10-338-044-386

Query Match Best Local Similarity 80.7%; Score 96.8; DB 8; Length 649; Matches 104; Conservative 89.7%; Pred. No. 5.6e-18; Mismatches 12; Indels 0; Gaps 0; Gaps 0; PCT-US03-01096-36

Sequence 15359 Application US/09947907
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: COLLECTION OF CODING REGION SINGLE NUCLEOTIDE POLYMORPHISM (SNP) LOCATED ON EACH OF THE HUMAN CHROMOSOMES, METHODS OF DETECTION, AND USES THEREOF
TITLE OF INVENTION: NUCLEOTIDE POLYMORPHISM (SNP) LOCATED ON EACH OF THE HUMAN CHROMOSOMES, METHODS OF DETECTION, AND USES THEREOF
FILE REFERENCE: CL000896
CURRENT APPLICATION NUMBER: US/09/947,907
CURRENT FILING DATE: 2003-03-17
PRIORITY APPLICATION NUMBER: 60/241,755
PRIORITY FILING DATE: 2000-10-20
PRIORITY APPLICATION NUMBER: 60/237,768
PRIORITY FILING DATE: 2000-10-03
PRIORITY APPLICATION NUMBER: 60/231,498
PRIORITY FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 21266
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15359
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-947-907-15359

RESULT 7
US-09-947-907-15359/c
Sequence 15359 Application US/09947907
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: COLLECTION OF CODING REGION SINGLE NUCLEOTIDE POLYMORPHISM (SNP) LOCATED ON EACH OF THE HUMAN CHROMOSOMES, METHODS OF DETECTION, AND USES THEREOF
FILE REFERENCE: CL000896
CURRENT APPLICATION NUMBER: US/09/947,907
CURRENT FILING DATE: 2003-03-17
PRIORITY APPLICATION NUMBER: 60/241,755
PRIORITY FILING DATE: 2000-10-20
PRIORITY APPLICATION NUMBER: 60/237,768
PRIORITY FILING DATE: 2000-10-03
PRIORITY APPLICATION NUMBER: 60/231,498
PRIORITY FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 21266
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15359
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-947-907-15359

Query Match Best Local Similarity 98.8%; Score 80.4; DB 5; Length 601; Matches 81; Conservative 90%; Mismatches 1; Indels 0; Gaps 0; Gaps 0; PCT-US03-01096-36

Sequence 1041 Application US/60443566
GENERAL INFORMATION:
APPLICANT: CARGIL, Michele
APPLICANT: BEGOVICH, Ann
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001447
CURRENT APPLICATION NUMBER: US/60/443,566
CURRENT FILING DATE: 2003-01-30
NUMBER OF SEQ ID NOS: 25102
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1041
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
US-60-443-566-1041

Query Match Best Local Similarity 100.0%; Score 61; DB 9; Length 201; Matches 99; Conservative 99%; Mismatches 0; Indels 0; Gaps 0; Gaps 0; PCT-US03-01096-36

Sequence 36 Application PC/TUS03/01096
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.; JONES, Anissa L.; DAHL, Christopher R.; GLETZEN, Darryl; CHINN, Joyce; DUFOUR, Gerard E.; JACKSON, Jennifer L.; YU, Jimmy Y.; TURSON, Olivia; YAP, Pierre E.; AMSHEY, Steffan R.; DAM, Tam C.; LIU, Tommy F.; GERTIN JR., Edward H.; PERALTA, Careyna H.; LEWIS, Samantha A.; CHEN, Alice; MARWAH, Rakesh; LAN, Ruth.; URASHKA, Michael; R., KRISTNAM, Sreenivasa R.; KOLLURU, Vijaykumar; PANISAR, Iqbal S.; TITLE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PT-139 PCT
CURRENT APPLICATION NUMBER: PCT/US03/01096
CURRENT FILING DATE: 2003-01-13
PRIORITY APPLICATION NUMBER: US 60/349,384
PRIORITY FILING DATE: 2002-01-16
PRIORITY APPLICATION NUMBER: US 60/349,946
PRIORITY FILING DATE: 2002-01-17
PRIORITY APPLICATION NUMBER: US 60/349,413
PRIORITY FILING DATE: 2002-01-17
NUMBER OF SEQ ID NOS: 377
SOFTWARE: PERL Program
SEQ ID NO 36
LENGTH: 1195
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: LG:776175.9:2002JAN18
PCT-US03-01096-36

Query Match Best Local Similarity 98.8%; Score 80.4; DB 1; Length 1195; Matches 81; Conservative 98.8%; Pred. No. 2.8e-13; Mismatches 1; Indels 0; Gaps 0; Gaps 0; PCT-US03-01096-36

Sequence 39 Application US/60443566
GENERAL INFORMATION:
APPLICANT: CARGIL, Michele
APPLICANT: BEGOVICH, Ann
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001447
CURRENT APPLICATION NUMBER: US/60/443,566
CURRENT FILING DATE: 2003-01-30
NUMBER OF SEQ ID NOS: 25102
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1041
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
US-60-443-566-1041

QY 60 CACTGAGGAGGACATGCCAGGAGGAAGGCCCTCCACCCACGGAGGAGCACACCTC 119
Db 1 CACTGAGGAGGACATGCCAGGAGGAAGGCCCTCCACCCACGGAGGAGCACACCTC 60

QY 120 C 120
Db 61 C 61

RESULT 10
US-10-266-131-2686
Sequence 2686 Application US/10266131
GENERAL INFORMATION:
APPLICANT: Friedrich, Glenn
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: Novel Murine Polynucleotide Tags and
FILE REFERENCE: LEX-0030-USA
CURRENT APPLICATION NUMBER: US/10/266,131
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: US/09/617,675
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 60/143,878
FILING DATE: 1999-07-15
NUMBER OF SEQ ID NOS: 2908
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 2686
LENGTH: 609
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(609)
OTHER INFORMATION: n = A,T,C or G

US-10-266-131-2686

Query Match Score 51.6; DB 8; Length 609;
Best Local Similarity 85.1%; Pred. No. 3.5e-05;
Matches 57; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 TCGCTGTGATGAGAAGTGACCTGAGGCCGATGAGGACCTGTGAGTGTAC 60
Db 543 TCCCTGTGATGAGAAGTACATCTGAGGACAGCGAGGACTGAGGATGAC 602

QY 61 ACTGAGG 67
Db 603 ACAGAGG 609

RESULT 11
US-10-388-360-334/c
; Sequence 334 Application US/10388360
GENERAL INFORMATION:
APPLICANT: GENOMIC HEALTH
APPLICANT: Baker, Joffre B.
APPLICANT: Cronin, Maureen T.
APPLICANT: Kieffer, Michael C.
APPLICANT: Shak, Steve
APPLICANT: Walker, Michael Graham
TITLE OF INVENTION: GENE EXPRESSION PROFILING IN BIOPSTED TUMOR TISSUES
FILE REFERENCE: 39740-0001US
CURRENT APPLICATION NUMBER: US/10/388,360
CURRENT FILING DATE: 2003-03-12
PRIOR APPLICATION NUMBER: US 60/412,049
PRIOR FILING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: US 60/364,890
PRIOR FILING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 384
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 334
LENGTH: 3373

RESULT 12
US-10-264-237-108/c
Sequence 1083 Application US/10264237
GENERAL INFORMATION:
APPLICANT: Bille et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA131P
CURRENT APPLICATION NUMBER: US/10/264, 237
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/16450
PRIOR FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: US 60/205,515
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 2876
SOFTWARE: Patentin Ver. 3.1
SEQ ID NO: 1083
LENGTH: 595
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (551)..(551)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (575)..(575)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (577)..(577)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (587)..(587)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (587)..(587)
OTHER INFORMATION: n equals a,t,g, or c

US-10-264-237-1083

Query Match Score 32.2; DB 8; Length 595;
Best Local Similarity 63.6%; Pred. No. 11; Mismatches 28; Indels 0; Gaps 0;
Matches 49; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 44 GGAACCTGTGAGACTGAGGACATGCCAGGAGAACGCTCCACCCACGGA 103
Db 463 GGACAGACGAGACTGGCACAGGGCACCGCGACAGGGCACGGCCACACAGA 404
QY 104 GGAGGAGGAGCACCTCC 120
Db 403 GGATGAGGGTCCTC 387

RESULT 13
US-60-452-680-6448/c
; Sequence 6448 Application US/60452680
GENERAL INFORMATION:
APPLICANT: Cargill, Michele
APPLICANT: Grube, Andrew

RESULT 14
 US-60-452-680-6447/C
 ; Sequence 6447, Application US/60452680
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: C1Q01450
 ; CURRENT APPLICATION NUMBER: US/60/452,680
 ; CURRENT FILING DATE: 2003-03-07
 ; NUMBER OF SEQ ID NOS: 116213
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO: 6448
 ; LENGTH: 891
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-60-452-680-6448

Query Match 26.8%; Score 32.2; DB 9; Length 891;
 Best Local Similarity 63.6%; Pred. No. 12; Mismatches 28; Indels 0; Gaps 0;
 Matches 49; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Qy 44 GGAACTGTGAGAGTGACACTGGAGGACATGCCAGGAGAAAGCCCTTACCCACGGA 103
 Db 327 GGAAACGACGACTGGACAGTGAGGTACCGGAGCAGGGCAGGCCACAGA 268

Qy 104 GGAGGAGGAGCACCTCC 120
 Db 267 GGATGAGCGGGCTTC 251

RESULT 15
 US-60-452-680-6447/C
 ; Sequence 6447, Application US/60452680
 ; GENERAL INFORMATION:
 ; APPLICANT: GRUPE, Andrew
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: C1Q01450
 ; CURRENT APPLICATION NUMBER: US/60/452,680
 ; CURRENT FILING DATE: 2003-03-07
 ; NUMBER OF SEQ ID NOS: 116213
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO: 6447
 ; LENGTH: 1160
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-60-452-680-6447

Query Match 26.8%; Score 32.2; DB 9; Length 1160;
 Best Local Similarity 63.6%; Pred. No. 13; Mismatches 28; Indels 0; Gaps 0;
 Matches 49; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Qy 44 GGAACTGTGAGAGTGACACTGGAGGACATGCCAGGAGAAAGCCCTTACCCACGGA 103
 Db 1318 GGAAAGCAGCACCTGCACTGAGGTACCGCGAGCACGGCCAGGCCACAGA 656

Qy 104 GGAGGAGGAGCACCTCC 120
 Db 1258 GGATGAGGGCTTC 1242

RESULT 16
 US-60-452-680-6447/C
 ; Sequence 6447, Application US/60452680
 ; GENERAL INFORMATION:
 ; APPLICANT: Teng, Y. Tom
 ; APPLICANT: Liu, Chenghua
 ; APPLICANT: Asundi, Vinod
 ; APPLICANT: Zhang, Jie
 ; APPLICANT: Ren, Feiyan
 ; APPLICANT: Chen, Rui-hong
 ; APPLICANT: Zhao, Qing A.
 ; APPLICANT: Wehrman, Tom
 ; APPLICANT: Xue, Aidong J.
 ; APPLICANT: Yang, Yonghong
 ; APPLICANT: Wang, Jian-Rui
 ; US-60-452-680-6447

Query Match 26.8%; Score 32.2; DB 6; Length 1923;
 Best Local Similarity 63.6%; Pred. No. 14; Mismatches 28; Indels 0; Gaps 0;
 Matches 49; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Qy 44 GGAACTGTGAGAGTGACACTGGAGGACATGCCAGGAGAAAGCCCTTACCCACGGA 103
 Db 1318 GGAAAGCAGCACCTGCACTGAGGTACCGCGAGCACGGCCAGGCCACAGA 656

Qy 104 GGAGGAGGAGCACCTCC 120
 Db 1258 GGATGAGGGCTTC 1242

Search completed: April 4, 2003, 22:50:28
 Job time : 66.8335 sec

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